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Om protein - protein search, using sw model.

Run on: January 6, 2002, 09:47:04 ; Search time 22.43 Seconds

(without alignments)
82.561 Million cell updates/sec

Title: US-09-441-061-2
perfect score: 125
Sequence: GMAALPRLIAFTSEHSHFSLRKGA 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 7407290 residues

Total number of hits satisfying chosen parameters:

220984

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A_Geneseq_1101:*

1: /SIDS2/gcgatata/geneseq/geneseq/AA1980.DAT:*

2: /SIDS2/gcgatata/geneseq/geneseq/AA1981.DAT:*

3: /SIDS2/gcgatata/geneseq/geneseq/AA1982.DAT:*

4: /SIDS2/gcgatata/geneseq/geneseq/AA1983.DAT:*

5: /SIDS2/gcgatata/geneseq/geneseq/AA1984.DAT:*

6: /SIDS2/gcgatata/geneseq/geneseq/AA1985.DAT:*

7: /SIDS2/gcgatata/geneseq/geneseq/AA1986.DAT:*

8: /SIDS2/gcgatata/geneseq/geneseq/AA1987.DAT:*

9: /SIDS2/gcgatata/geneseq/geneseq/AA1988.DAT:*

10: /SIDS2/gcgatata/geneseq/geneseq/AA1989.DAT:*

11: /SIDS2/gcgatata/geneseq/geneseq/AA1990.DAT:*

12: /SIDS2/gcgatata/geneseq/geneseq/AA1991.DAT:*

13: /SIDS2/gcgatata/geneseq/geneseq/AA1992.DAT:*

14: /SIDS2/gcgatata/geneseq/geneseq/AA1993.DAT:*

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18: /SIDS2/gcgatata/geneseq/geneseq/AA1997.DAT:*

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21: /SIDS2/gcgatata/geneseq/geneseq/AA2001.DAT:*

22: /SIDS2/gcgatata/geneseq/geneseq/AA2002.DAT:*

ALIGNMENTS

RESULT 1

ID AAR88667 standard; peptide; 25 AA.

XX AC AAR88667;

XX DT 05-MAR-1996 (first entry)

XX DE Human glutamic acid decarboxylase residues 266-290.

XX KW diabetes; T-cell subpopulation; detection; antigen production;

XX KW diagnosis; autoimmune disease.

XX OS Homo sapiens.

XX PN DE4418091-A1.

PD 27-JUL-1995.

XX PF 24-MAY-1994; 94DE-4418091.

XX PR 04-FEB-1994; 94DE-4403522.

PR 20-JAN-1994; 94DE-4401629.

XX PA (ENDL/ ENDL J.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX PT Albert W, Dornmair K, Endl J, Jung G, Meinl E;

PI Stahl P, Schendel D;

Republis C virus

Hepatitis C virus

HCV NS peptide DP3

Rheumatoid arthrit

Hepatitis C virus

Hepatitis C virus

Hepatitis C virus

Hepatitis C virus

HCV peptide NS4e

HCV antigen NS4 1

HCV type 16 antig

ICM-3 P20 region 1

HTLV-PX-related pe

Sequence 2 encoded

HLA-DR beta-chain

AV37 antigen prote

Glutamic acid deca

Human chorionic go

Human choriocarcin

HTV-1 group O stra

Fragment of human

Peptide #727 encod

Peptide #740 encod

Human cDNA partial

Peptide #704 encod

HCV type 16 antig

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	125	100.0	25	16 AAR88667	Human glutamic aci
2	125	100.0	25	18 AAW18848	65 kd Glutamic aci
3	82	65.6	20	16 AAR72279	Glutamic acid deca
4	82	65.6	20	21 AAY59552	GAD65 fragment, pe
5	67	53.6	20	16 AAR72278	Glutamic acid deca
6	67	53.6	20	21 AAY59578	GAD65 fragment, pe
7	64	51.2	20	21 AAY57065	Glutamate decarbox
8	39	31.2	24	21 AAB07785	Glutamic acid deca
9	37	30.9	15	22 ABA6152	HCV type 16 antig
10	37	29.6	15	19 AAW5435	Helper T-cell clas
11	37	29.6	15	21 AAY73095	Hepatitis C virus

XXX WPI; 1995-264505/35.

XXX DDR

XXX PCT Antigen-specific activated T-lymphocytes and their detection - by
XXX PCT interaction with inventive peptide(s) of peptide-MHC complexes;
XXX PCT used in diagnosis of e.g. diabetes and auto-immune diseases

XXX PPS Claim 1; Page 13; 21PP; German.

XXX PPS *ARR8667* is derived from residues 266-290 of human glutamic acid
XXX PPS decarboxylase and specifically reacts with a T-cell sub-population
XXX PPS isolated from recently diagnosed Type-I diabetics. Pharmaceutical
XXX PPS compounds, contg. this peptide and those shown in ARR8668 and
XXX PPS ARR76612-62, are useful for the diagnosis of a disease or predisposition
XXX PPS of immune system diseases, tumours, and autoimmune diseases, including
XXX PPS diabetes. The peptides are able to detect specific T-cell subpopulations
XXX PPS that are then used for antigen prodn., e.g. by reinjection.

XXX Sequence 25 AA;

XXX SQ

Query	Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1	GMAALPRLIAFTSRSRSHFSLLKKGAA	25		100.0%	Score 125;	DB 16;	Length 25;	0;
D _b		1 qmaalpriaftsrsrhfsllkkgaa	25		100.0%	Pred. No. 8.5e-15;	0;	0;	0;

RESULT	2
AAW18848	
ID	AAW18848 standard; peptide; 25 AA.
XX	
XX	AAW18848;
XX	
DDT	05-JAN-1998 (first entry)
XX	
DE	65 kd Glutamic acid decarboxylase peptide fragment VII.
XX	
KW	GAD: 65 kd; human: glutamic acid decarboxylase; autoreactive; diagnosis;
KW	insulin dependent diabetes mellitus; IDDM; cell mediated disease;
KW	predisposition; autoimmune; tumour; rheumatoid arthritis;
KW	multiple sclerosis.

AA	OS	Synthetic.	
XX	XX		
XX	PN	DE19526561-A1.	
XX	PD	23-JAN-1997.	
XX	PP	20-JUL-1995;	95DE-1026561.
XX	PR	20-JUL-1995;	95DE-1026561.
XX	PA	(BOEF) BOEHRINGER MANNHEIM GMBH.	
XX	PI	Donie F, Endl J, Ganz M, Jung G,	Klientesch-engel R;
XX	PI	Pozzilli P, Stahl P;	
XX	DR		
XX	PT	WPI; 1997-088254/09.	Skin test for diagnosis of cell-mediated diseases, esp.

XX Claim 11; Page 10; 12pp; German.
PS
XX AAV18842-70 are peptide fragments of the 65 kD human glutamic acid
CC carboxypeptidase (GAD). The fragments are auto-reactive substances used for
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis
CC is determined by using a claimed method for diagnosis of cell-mediated
CC diseases or a predisposition to cell-mediated diseases, which is
CC effected by administering an auto-reactive substance intradermally and
CC

CC establishing the diagnosis on the basis of the occurrence or lack of a positive reaction at the site of administration. The method is used for diagnosis of autoimmune and tumour diseases, preferably T-cell-mediated diseases such as rheumatoid arthritis, multiple sclerosis and especially IDDM.

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Query Match          100.0%;   Score 125; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy   1 GMAALPRLIAFTSEHSHSFLKGA 25
Db   1 gmaalprliaftsehshfslkcaa 25

```

AAR72279 standard; Peptide; 20 AA.
 ID AAR72279
 XX AC AAR72279;
 XX DT 13-NOV-1995 (first entry)
 XX DE Glutamic acid decarboxylase (GAD65)
 XX

KW insulin-dependant diabetes mellitus; stiff man disease.
 XX OS Homo sapiens.
 XX PN KW0507992-A.
 XX PD 23-MAR-1995.
 XX PF 24-AUG-1994; 94WO-US09478.
 XX PR 17-SEP-1993; 93US-0123859.
 XX PA (REGC) UNIV CALIFORNIA.
 XX Clare-Salzler NJ, Erlander MG, Kaufman DL, Tobin AJ;

DR	WP; 1995-131360/17.
XX	New polypeptide fragments of glutamic acid decarboxylase - for diagnosis and treatment of auto immune disease, esp. insulin dependent diabetes, also related nucleic acid, vectors, antibodies, hybridomas) etc.
XX	Example 11; Page 76; 100pp; English.
PS	AA086481 and AA086482 encode AAR71173 and AAR79105, rat and human glutamic acid decarboxylase (GAD65) respectively, from which the fragments described in AAR7261-R72298 were derived. These fragments can be used to detect autoantibodies against GAD, e.g. to diagnose and treat GAD-related autoimmune disorders, such as insulin dependant diabetes mellitus or stiff man disease.
XX	Sequence 20 AA;

RESULT 4
 AAY59552 standard; peptide; 20 AA.
 XX
 AC
 XX
 DT 03-APR-2000 (first entry)
 XX
 DE GAD65 fragment, peptide #19.
 XX
 KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependant diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5998366-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 09-APR-1997; 97US-0827618.
 XX
 PR 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0580536.
 PR 18-JUN-1991; 91US-0716909.
 PA (REGC) UNIV CALIFORNIA.
 PI Tobin AJ, Kaufman DL, Erlander MG;
 DR WPI; 2000-095930/08.
 XX
 PT Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependant diabetes mellitus and stiff man
 disease.
 XX
 PS Claim 1; Column 42; 61pp; English.
 XX
 CC This sequence represents a fragment of the glutamic acid decarboxylase 65
 (GAD65) protein. The invention relates to a method of ameliorating GAD
 associated autoimmune disorders by administering a GAD65 peptide to the
 patient. The method can be used for ameliorating GAD associated
 autoimmune disorders such as IDDM (insulin dependant diabetes mellitus)
 and Stiff man disease. GAD65 can also be useful for screening drugs that
 alter GAD function, for generating monoclonal antibodies and in
 immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 and the diagnosis is quite easy. It is also possible to obtain much
 larger quantities of polypeptides via recombinant techniques than are
 available from natural sources.
 XX
 Sequence 20 AA;
 XX
 Query Match 53.6%; Score 67; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.6e-05; Mismatches 0;
 Matches 14; Conservative 0; Indels 0; Gaps 0;
 Db 7 gmaalpilafuse 20
 RESULT 6
 OY 1 GMALALPRLIAFUSE 14
 |||||||
 ID AAY59578 standard; peptide; 20 AA.
 XX
 AC AAY59578;
 XX
 DT 03-APR-2000 (first entry)
 XX
 DE GAD65 fragment, peptide #18.
 XX
 KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependant diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5998366-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 09-APR-1997; 97US-0827618.
 XX
 PR 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0580536.
 PR 18-JUN-1991; 91US-0716909.
 PA (REGC) UNIV CALIFORNIA.
 PI Tobin AJ, Kaufman DL, Erlander MG;

XX WPI; DR 2000-095930/08.
XX Ameliorating glutamic acid decarboxylase associated autoimmune
XX disorders such as insulin dependent diabetes mellitus and Stiff man
XX disease -
XX Example 11; Column 42; 61pp; English.
XX This sequence represents a fragment of the glutamic acid decarboxylase
XX (GAD65) protein. The invention relates to a method of ameliorating GAD
XX associated autoimmune disorders by administering a GAD65 peptide to the
XX patient. The method can be used for ameliorating GAD associated
XX autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
XX and Stiff man disease. GAD65 can also be useful for screening drugs that
XX alter GAD function, for generating monoclonal antibodies and in
XX immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
XX and the diagnosis is quite easy. It is also possible to obtain much
XX larger quantities of polypeptide via recombinant techniques than are
XX available from natural sources.
XX Sequence 20 AA:
XX

```

Query Match      53.6%; Score 67; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACC 1 GMAALPRLAFTSE 14

```

antigen based immunotherapeutic agent, to a host afflicted with an autoimmune response associated with an autoimmune disease. The immunotherapeutic agent is used to treat autoimmune diseases such as insulin dependent diabetes mellitus, multiple sclerosis, autoimmune thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal inflammatory immune responses. The NTTA induces regulatory tolerance by elicitation of regulatory T cells among T cells recognizing the NTTA but not participating in the immune response. The NTTA are capable of recognition by substantial populations of uncommitted T cells which can be primed, or biased, towards regulatory responses to provide effective treatment. The NTTA are effective in regulating undesirable immune responses even when target determinants used as agents promoting tolerance agents have failed to induce an effective regulatory T cell response. NTTAs as agents promoting tolerance are anticipated to be safer than use of target determinants.

1 GMAALPRLAFTSE 14
 | | | | | | | |
 7 gmaavprlaftse 20

 DULT 8

 07785 AAB07785 standard; peptide; 24 AA.

 AAB07785;

 07-NOV-2000 (first entry)

 Glutamic acid decarboxylase-65 (GAD-65) analogue peptide.

 Glutamic acid decarboxylase-65; GAD-65; autoimmune disease;
 insulin-dependent diabetes mellitus; IDDM; stiff man syndrome;
 cellular autoimmune response; T-cell receptor; autoimmune antigen.

 Synthetic.

Key	Location/Qualifiers
Misc-difference	15
	/label= Thr, Glu

 EP1026238-A2.

 09-AUG-2000.

 17-JUN-1992; 20000EP-0102269.

 18-JUN-1991; 91US-0716909.

 17-JUN-1992; 92EP-0110308.

 (REGC) UNIV CALIFORNIA.

 Tobin AJ, Erlander MG, Kaufman DL, Clare-salzler MJ;

 WPI; 2000-500251/45.

 Claim 15; Page -; 32pp; English.

The specification describes a method which uses a glutamic acid decarboxylase-65 (GAD-65) polypeptide or analogue for diagnosing and treating autoimmune diseases such as insulin-dependent diabetes mellitus and detecting antibodies to glutamin acid decarboxylase (GAD)65 in a sample, using GAD65 polypeptide.

CC for the preparation of medicament for treating IDDM or stiff man syndrome, detecting antibodies (preferably autoantibodies to GAD-65).
 CC It is also useful for classifying patients with autoimmune diseases such as IDDM, screening drugs that alters GAD function, generation of an antibody preferably monoclonal or polyclonal autoantibodies, blocking cellular autoimmune response, blocking recognition by a specific T-cell receptor or an major histocompatibility complex (MHC) receptor presenting an autoimmune antigen on the surface of an antigen presenting cell, stimulating a T-suppressor cell population, and competing for recognition of self-antigens at a level of antigen presentation. The present sequence represents a GAD-65 analogue of the invention.
 CC note: the present sequence does not appear in the specification; it was created using information provided.

XX Sequence 24 AA;
 SQ

Query Match 31.2%; Score 39; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMALAPRL 8
 DB 17 gmalaprl 24

RESULT 9
 AAB46152 standard; peptide; 15 AA.
 ID AAB46152

XX AAB46152;
 AC XX

DT 04-APR-2001 (first entry)
 XX

DE HCMV type 16 antigenic peptide SEQ ID NO 20.
 XX

KW Antigenic; vaccine; interferon-gamma; tumor necrosis factor-alpha;
 KW CD8+ T cell; hCMV infection; immune response.

OS Human cytomegalovirus.
 XX

PN WO200075180-A2.

XX PD 14-DEC-2000.

XX PR 02-JUN-2000: 2000WO-DE01854.

XX PR 04-JUN-1999: 99WO-1027039.

XX PR 07-SEP-1999: 99WO-1043702.

XX PA (KERN/) KERN F.

XX PI Kern F., Volk H., Reinke P., Faulhaber N., Surel I., Khatamzas E;

XX DR XX

DR WPI: 2001-061700-07.

XX New peptides that stimulate cytokine production in T cells, useful for vaccination against human cytomegalovirus infection and for detecting immune responses to the virus

XX claim 1, Page 26, 28pp; German.

XX This invention describes novel peptides (I), their encoding DNA (II) or

CC therapeutic or prophylactic vaccination against hCMV infection and as diagnostic reagents for detecting or quantifying the cellular immune

CC response to hCMV (from ability to induce production of the specific

CC cytokines in CD8+ cells), particularly in immune-deficient subjects. Also

CC DNAs (II) that encode (I), and vectors and plasmids containing (II), are

CC useful as pharmaceuticals.

XX	SQ	Sequence	15 AA;
Query Match 30.0%; Score 37.5; DB 22; Length 15;	Best Local Similarity 66.7%; Pred. No. 7.1; Mismatches 2; Indels 1; Gaps 1;		
OY 9 IAFTSBSSHSSL 20	DB 2 vafts-hehgql 12		
RESULT 10	AAW85435	ID AAW85435 standard; peptide; 15 AA.	
XX AC AAW85435;	XX DT 16-FEB-1999 (first entry)		
XX DE Helper T-cell class II peptide derived from NS4 protein.	XX KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7; cytotoxic T lymphocyte; CTL; hepatitis; malaria; cancer; acquired immune deficiency syndrome; Lyme disease; hepatitis; allograft rejection; allergy; post-streptococcal endocarditis; glomerulonephritis; food hypersensitivity.		
XX OS Synthetic. OS Hepatitis C virus.	XX PF 23-JAN-1998; 99WO-US01373.		
XX PN WO9832456-A1.	XX PR 07-FEB-1997; 97US-0037432.		
XX PD 30-JUL-1998.	PR 23-JAN-1997; 97US-0036713.		
XX PA (EPIM-) EPIMUNE INC.	XX DR		
XX Sette A., Sidney J., Southwood S;	XX WPI: 1998-427679/36.		
XX PT Composition containing peptide that induces cytotoxic T lymphocyte response, and helper peptide can bind to human leucocyte antigen alleles, used to treat or prevent cancers, parasitic infections and autoimmune disease.	XX PS Disclosure; Page 42; 51pp; English.		
XX DR AAW85284-451 represent helper T-cell class II peptides, which can bind to the human leucocyte antigens (HLA) DR4w, DR1 and DR7. The peptides are used in the course of the invention. The specification describes peptides that that induce a cytotoxic T lymphocyte (CTL) response, and T-helper peptides, that are used together to generate a CTL response for the treatment or prevention of viral, fungal, bacterial or parasitic infections (e.g. hepatitis, acquired immune deficiency syndrome or malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate cancer or condyloma acuminatum). Helper T-cell peptides may be used alone to induce a helper T cell response, e.g. in cases of autoimmune disease, allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal endocarditis, glomerulonephritis and food hypersensitivity.	XX SQ Sequence 15 AA;		

Query Match

29.6%; Score 37; DB 19; Length 15;

Best Local Similarity 61.5%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Score 37; DB 21; Length 15;

QY 7 RLIAFTSEHSHFS 19
XX 1|1|| | :| |
DB 3 rliafasrgnhs 15

RESULT 11 :
AAV73095 standard; Peptide: 15 AA.

ID AAV73095
XX
AC AAW73055;
DT 28-FEB-2000 (first entry)
DE Hepatitis C virus (HCV)-derived MHC class II (HTL) epitope, #253.
XX Chimeric; pan DR epitope; expression vector; MHC; targeting; peptide; promoter; major histocompatibility complex; MHC; targetting; peptide; epitope; antigen; presentation; class I; cytosolic pathway; endoplasmic reticulum; class II; extracellular antigen; cytotoxic T lymphocyte; helper T lymphocyte; HTL; universal epitope; vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV; hepatitis B; hepatitis C; bacterium; protozoan; tumour cell; autoimmune disease; activation; antiviral; antimarial; immunoprotective.

XX Synthetic.
OS Hepatitis C virus.
XX WO9958658-A2.
PN XX
PD 18-NOV-1999.
XX PP 13-MAY-1999; 99WO-US10646.
PR 13-MAY-1998; 98US-0078904.
PR 15-MAY-1998; 98US-0055751.
PA (EPIM-) EPIMMUNE INC.
XX Flakes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B,
PI PI
DR Chestnut RW;
XX WPI; 2000-039103/03.
PT Expression vectors encoding major histocompatibility targeting sequence, used as, e.g. tumor vaccines -
XX Claim 11; Page 67; 130pp; English.
PS Sequences AAV73087-Y73102 represent hepatitis C virus (HCV)-derived MHC class II (HTL) epitopes which are claimed for use in the present invention. The invention relates to a novel expression vector comprising a promoter operably linked to a fusion gene encoding a major histocompatibility complex (MHC) targeting sequence and two or more heterologous peptide epitopes. The MHC targeting sequence may be a class I targeting sequence, which directs an MHC class I epitope to a cytosolic pathway or to the endoplasmic reticulum, or an MHC class II targeting sequence, which directs extracellular antigens to enter the endocytic pathway to be processed into antigen peptides for presentation on MHC class II molecules. The heterologous epitopes may comprise either helper T lymphocyte (HTL) epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL epitope such as a pan DR epitope (PADRE). The vectors are useful for stimulating an immune response *in vivo*, as well as for use in assaying the human immunogenicity of a human T cell peptide epitope *in vivo* in a non-human mammal. They provide a nucleic acid vaccine for enhancing immunity against infectious pathogens, such as viruses (e.g., HCV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g., Plasmodium falciparum, the cause of malaria) and also tumour cells and

CC autoimmune diseases. Universal MHC class II epitopes are advantageously combined with other MHC Class I and Class III epitopes to increase the number of cells that are activated in response to a given antigen and provide a broader population coverage of MHC-reactive alleles.

XX SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 21; Length 15;
Best Local Similarity 61.5%; Pred. No. 8.7;
Matches 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSHFS 19
Db 3 rliafasrgnhs 15.

RESULT 12
AAJ03084
ID AAJ03084 standard; Peptide: 15 AA.

XX
AC AAJ03084;
XX DT 02-JUL-2001 (first entry)
DE Hepatitis C virus epitope #3075.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif; antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
PS Disclosure; Page 174; 214pp; English.
XX WPI; 2001-308046/32.
XX PT A new composition useful as a vaccines against hepatitis C virus -
XX Disclosure; Page 174; 214pp; English.
PS The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ03010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
Best Local Similarity 61.5%; Pred. No. 8.7;
Matches 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSHFS 19
Db 3 rliafasrgnhs 15.

RESULT 13
AAJ03390
ID AAJ03390 standard; Peptide: 15 AA.

XX

AC AAJ03390;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #3381.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PR 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Example 5; Page 198; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared hepatitis C Virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in CC vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
 Best Local Similarity 61.5%; Pred. No. 8.7; Mismatches 4; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 XX
 PT Disclosure; Page 177; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in CC vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 15 AA;

RESULT 15
 AAJ04073
 ID AAJ04073 standard; Peptide: 15 AA.
 XX
 AC AAJ04073;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #4064.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PR 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.

PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Example 5; Page 201; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in CC vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 29.6%; Score 37; DB 22; Length 15;
 Best Local Similarity 61.5%; Pred. No. 8.7; Mismatches 4; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIJAFSEHSHFS 19
 1|1|| | :| |
 Db 3 rliafaargnvs 15

RESULT 16
 AAW01981
 ID AAW01981; standard; peptide; 20 AA.
 XX
 AC AAW01981;
 XX
 DT 26-SEP-1996 (first entry)
 DE Antigenic peptide comprising HCV NS4 protein residues 1916-1935.
 XX
 KW Antigenic peptide; C-terminal region; hepatitis C virus; HCV;
 KW non-A non-B; non-structural protein 4; NS4; differential diagnosis;
 KW acute; chronic; infection; binding assay.
 XX
 OS Hepatitis C virus.
 XX
 PN W09604300-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-US09599.
 PR 29-JUL-1994; 94US-0282758.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US SEC DEPT HEALTH.
 XX
 PI Fields HA, Khudyakov YE;
 XX
 DR WPI; 1996-129330/13.
 XX
 PT Antigenic peptide(s) binding anti-hepatitis C virus antibodies
 PT useful for differential diagnosis of HCV in subjects
 XX
 PS Claim 3; Page 27; 50pp; English.

The present peptide is an antigenic peptide (AP), derived from the C-terminal region of the hepatitis C virus (HCV) non-structural protein 4 (NS4). The AP was prepared using Fmoc chemistry, and can be used in a claimed method for the differential diagnosis of HCV. One, two or three of the peptides AAW01980-82 are separately contacted with an antibody (Ab) control sample, and the binding between the peptide(s) and the Ab determined. The Ab control sample is then contacted with the peptide AAW01983, and the binding between the peptide and the Ab determined. The strength of the binding between the peptide(s) and the Ab in the two assays is compared, where stronger binding in the 1st assay is indicative of acute HCV infection, and equivalent binding is indicative of chronic HCV infection.

Sequence 20 AA;

Query Match 29.6%; Score 37; DB 17; Length 20;
 Best Local Similarity 61.5%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIJAFSEHSHFS 19
 1|1|| | :| |
 Db 3 rliafaargnvs 15

RESULT 17
 AAY73093
 ID AAY73093 standard; Peptide; 22 AA.
 XX
 AC AAY73093;

XX 28-FEB-2000 (first entry)
 DT Hepatitis C virus (HCV)-derived MHC class II (HTL) epitope, #251.
 XX
 DE Chimeric; pan DR epitope; expression vector; MHC; targetting; peptide; promoter; major histocompatibility complex; MHC; targetting; peptide; epitope; antigen; presentation; Class I; cytosolic pathway;
 KW endoplasmic reticulum; class II; extracellular antigen; endocytic pathway; helper T lymphocyte; HML; universal epitope;
 KW cytotoxic lymphocyte; CTL; immune response; immunogenicity; assay;
 KW vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;
 KW hepatitis B; hepatitis C; bacterium; protozoan; tumour cell; autoimmune disease; activation; antiviral; antimalarial;
 KW immunoprotective.
 XX
 Synthetic.
 OS Hepatitis C virus.
 XX
 PN W09958658-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 13-MAY-1999; 99WO-US10646.
 XX
 PR 13-MAY-1998; 98US-0078904.
 PR 15-MAY-1998; 98US-0085751.
 XX
 PA (EPMN-) EPIMUNE INC.

Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
 Chesnut RW;
 WPI; 2000-039103/03.
 XX
 Expression vectors encoding major histocompatibility targeting sequence, used as, e.g. tumor vaccines -
 PT
 PI
 PI
 DR
 XX
 PA
 XX
 PS Claim 11; Page 67; 130pp; English.

Sequences AAY73087-Y73102 represent hepatitis C virus (HCV)-derived MHC class II (HTL) epitopes which are claimed for use in the present invention. The invention relates to a novel expression vector comprising a promoter operably linked to a fusion gene encoding a major histocompatibility complex (MHC) targeting sequence, and two or more heterologous peptide epitopes. The MHC targeting sequence may be a class I targeting sequence, which directs an MHC class I epitope to a cytosolic pathway or to the endoplasmic reticulum, or an MHC class II targeting sequence, which directs extracellular antigens to enter the endocytic pathway to be processed into antigen peptides for presentation on MHC class II molecules. The heterologous epitopes may comprise either helper T lymphocyte (HTL) epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL epitope such as a pan DR epitope (PADRE). The vectors are useful for stimulating an immune response *in vivo*, as well as for use in assaying the human immunogenicity of a human T cell peptide epitope *in vivo* in a non-human mammal. They provide a nucleic acid vaccine for enhancing immunity against infectious pathogens, such as viruses (e.g., HIV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g., Plasmodium falciparum, the cause of malaria) and also tumour cells and autoimmune diseases. Universal MHC class II epitopes are advantageously combined with other MHC class I and class II epitopes to increase the number of cells that are activated in response to a given antigen and provide a broader population coverage of MHC-reactive alleles.

Sequence 22 AA;

SQ

Query Match 29.6%; Score 37; DB 21; Length 22;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLIJAFSEHSHFS 19
 1|1|| | :| |
 Db 3 rliafaargnvs 15

AC AAY73093;

Db ||||| :| | 10 rliafasrgnvhvs 22

RESULT 18

AAR34072
ID AAR34072 standard; Peptide; 22 AA.
XX
AC
XX
DT 02-JUL-2001 (first entry)
DE Hepatitis C virus epitope #4063.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 200000-US19774.
XX
PR 19-JUL-1999; 990US-0357737.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Slaney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.

PT A new composition useful as a vaccines against hepatitis C virus -
XX
PS Example 5; Page 201; 214pp; English.

CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAR340010-AAR3404121.
CC These are derived from HCV HKA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 22 AA;

Query Match 29.6%; score 37; DB 14; Length 24;
Best Local Similarity 61.5%; Pred. No. 15; Mismatches 8; Indels 0; Gaps 0;
Matches 8; Conservative 1; Gaps 0;

Qy ||||| :| | 7 RIAFTSEHSHTS 19
Db 2 rliafasrgnvhvs 14

RESULT 20

AAY41898
ID AAY41898 standard; Peptide; 19 AA.
XX
AC AAY41898;
XX
DT 09-DEC-1999 (first entry)

DE Rheumatoid arthritis diagnostic protein isoform peptide #49.
XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW rheumatoid arthritis diagnostic protein isoform; screening;
KW expression reference protein isoform; prognosis.
XX
OS Homo sapiens.
XX
PN WO9947925-A2.
XX
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99WO-GB00763.
XX
PR 13-MAR-1998; 98GB-0005477.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parkh RB, Patel TP, Townsend RR;
XX
DR WPI; 1999-571871/48.
XX
PT Diagnosis of human rheumatoid arthritis by two-dimensional
PT electrophoresis
XX
PS Disclosure; Page 18; 157pp; English.
XX
PN WO9306888-A.
XX
OS Synthetic.
XX
PD 01-APR-1993.

XX
PF 16-SEP-1992; 92WO-US07865.
XX
ID 16-SEP-1991; 91US-0762135.
PR 12-FEB-1992; 92US-0835717.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Burk KH, Dreesman GR, Pauletti D;
XX
DR WPI; 1993-11737/14.
XX
PT Detection of hepatitis C virus antigens - using HCV reactive
PT antibody bound to solid support and competitive HCV
PT antigen-reporter complex
XX
PS Claim 27; Page 122; 190pp; English.
XX
CC The synthetic peptide corresponds to residues 1917-1940 of the NS4
CC domain of HCV. The peptide may be used for the sensitive and
CC specific detection of HCV infection. Antibodies raised against the
CC peptide can be used for passive immuno-prophylaxis and the HCV
CC antigens can be used in vaccines to prevent HCV infection.
See also AAR34041-65.
XX
SQ Sequence 24 AA;

CC A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of each chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIS), and for production of antibodies to RPIS. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AAY4184 to AAU42100 represent RP1 peptides, AAU42101 to AAU25066 to AAU25068 represent expression reference protein isoform peptides and CC used in the exemplification of the present invention.

XX Sequence 19 AA;

Query Match 28.0%; Score 35; DB 20; Length 19;
Best Local Similarity 43.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
SQ Sequence 11 AA;

QY 8 LIAFTSEHFKKG 23
||: :||: |: |
Db 1 lisvdtdhsnlylqng 16

RESULT 21

AAJ02448 standard; Peptide: 11 AA.

AC AAJ02448;

DT 02-JUL-2001 (first entry)

XX Hepatitis C virus epitope #2439.

DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;

KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;

KW antiviral.

OS Hepatitis C virus.

XX Sidney J., Southwood S., Livingston BD, Chesnut R.

PN WO200121189-A1.

XX DR 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 169; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

CC vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.

CC XX Sequence 11 AA;

Query Match 27.2%; Score 34; DB 22; Length 11;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLIAFTSEHSH 17
||||| |:
Db 1 rliafasrgnh 11

RESULT 22

AAJ02837 standard; Peptide: 11 AA.

ID AAJ02837

XX AC AAJ02837;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #2828.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;

KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX XX PD 29-MAR-2001.

XX PF 19-JUL-1999; 99US-0357737.

XX PR WPI; 2001-308046/32.

XX PA (EPIM-) EPIMMUNE INC.

XX PA (EPIM-) EPIMMUNE INC.

XX PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 169; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

PI Baker DM, Oelis E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus

XX Disclosure: Page 160; 214pp; English.

PS Sette A, Sidney J., Southwood S., Livingston BD, Chesnut R;

ID AAB82059 standard; peptide; 21 AA.
 XX
 AC AAB82059;
 XX
 AC
 DT 22-JUN-2001 (first entry)
 XX
 DE HCV antigen, NS4 1909-1929.
 XX
 KW Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
 KW viral infection.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200124822-A2.
 XX
 PD 12-APR-2001.
 XX
 PP 02-OCT-2000; 2000WO-EP09657.
 XX
 PR 01-OCT-1998; 99AT-0001680.
 XX
 PA (CIST -) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Fleitmann J, Mattner F, Buschle M, Mellink J;
 XX
 DR WPI; 2001-290577/30.
 XX
 PT New pharmaceutical composition comprising an antigen, an
 PT immunostimulating substance and a polycationic polymer, useful in
 PT manufacturing vaccines
 XX
 PS Claim 12; Page 16; 20pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 CC (a) an antigen; (b) an immunostimulating substance consisting of
 CC neuroactive compounds, hormones, compounds having growth hormone activity
 CC or their mixtures; and (c) a polycationic polymer. The present sequence
 CC is an antigenic peptide derived from Hepatitis C virus, which was used in
 CC the present invention. The composition is useful in manufacturing
 CC vaccines.
 XX
 SQ Sequence 21 AA;

Query Match 27.2%; Score 34; DB 22; Length 21;
 Best Local Similarity 63.6%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 7 RLIATSEHSH 17
 Db 10 rliafasrqnh 20

Search completed: January 6, 2002, 09:51:45
 Job time: 281 sec

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29	31	24.8	13	4	PCT-US08411-727-4	Seq.
30	31	24.8	15	4	US-08-908-436-7	Seq.
31	31	24.8	18	2	US-08-480-190-79	Seq.
32	31	24.8	18	2	US-08-480-379-79	Seq.
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34	30	24.0	9	3	US-08-159-339-1008	Seq.
35	30	24.0	9	3	US-08-159-339-1009	Seq.
36	29	23.2	10	2	US-08-107-676-5	Seq.
37	29	23.2	10	3	US-08-159-339A-962	Seq.
38	29	23.2	11	3	US-08-467-580-69	Seq.
39	29	23.2	11	5	PCT-US95-08516-69	Seq.
40	29	23.2	14	1	US-07-909-122-16	Seq.
41	29	23.2	20	1	US-07-679-974D-5	Seq.
42	29	23.2	20	1	US-08-199-508-7	Seq.
43	29	23.2	20	2	US-08-934-915-117	Seq.
44	29	23.2	20	2	US-08-934-915-145	Seq.
45	29	23.2	20	2	US-08-945-168-10	Seq.
46	29	23.2	22	3	US-09-093-222-75	Seq.
47	29	23.2	23	3	US-09-093-222-75	Seq.
48	28	22.8	21	4	US-08-143-124-22	Patent
49	28	22.4	11	3	US-08-467-580-0	Sequence
50	28	22.4	11	5	PCT-US95-08516-30	Sequence
ALIGNMENTS						
Description						
RESULT	1					
; Sequence	32, Application US/08484530					
Patent No.	5846740					
GENERAL INFORMATION:						
APPLICANT:	Tobin, Allan J					
APPLICANT:	Erlander, Mark G					
APPLICANT:	Kaufman, Daniel L.					
TITLE OF INVENTION:	Cloned Glutamic Acid Decarboxylase					
NUMBER OF SEQUENCES:	60					
CORRESPONDENCE ADDRESS:						
ADDRESSEE:	Flehr, Hohbach, Test, Albritton & Herbert					
STREET:	Four Embarcadero Center, Suite 3400					
CITY:	San Francisco					
STATE:	CA					
COUNTRY:	US					
ZIP:	94111-4187					
COMPUTER READABLE FORM:						
MEDIUM TYPE:	FLOPPY disk					
COMPUTER:	IBM PC compatible					
OPERATING SYSTEM:	PC-DOS/MS-DOS					
SOFTWARE:	Patent Release #1.0, Version #1.30					
CURRENT APPLICATION DATA:						
APPLICATION NUMBER:	US/08/484,530					
FLILING DATE:	07-JUN-1995					
CLASSIFICATION:	435					
ATTORNEY/AGENT INFORMATION:						
NAME:	Trecartin, Richard F.					
REGISTRATION NUMBER:	31,801					
REFERENCE/DOCKET NUMBER:	A-60780-8/REF/MTK					
TELECOMMUNICATION INFORMATION:						
TELEPHONE:	415-398-1989					
TELEFAX:	415-398-3249					
INFORMATION FOR SEQ ID NO:	32:					
SEQUENCE CHARACTERISTICS:						
LENGTH:	20 amino acids					
TYPE:	amino acid					
STRANDEDNESS:	single					
TOPOLOGY:	linear					
MOLECULE TYPE:	peptide					
; US-08-484-530-32						
Query Match Local Similarity	65.6%; Score 82; DB 2; Length 20;					
Best Local Similarity	100.0%; Pred. No. 7.4e-08;					

RESULT ²
 US-08-827-618A-32
 Sequence 32, Application US/08827618A
 Patent No. 598366
 GENERAL INFORMATION:
 APPLICANT: Tobin, Allan J
 ERLANDER, Mark G
 ATTORNEY/AGENT INFORMATION:
 KAUFMAN, Daniel L.
 TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/827,618A
 FILING DATE: 09-APR-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/827,618A
 FILING DATE: 09-APR-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,725
 FILING DATE: 07-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/07/16,909
 FILING DATE: 18-JUN-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/07/586,536
 FILING DATE: 21-SEP-1990
 PRIORITY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-398-3249
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-827-618A-32
 RESULT ³
 US-08-484-952A-32
 Sequence 32, Application US/08484530
 Patent No. 611139
 GENERAL INFORMATION:
 APPLICANT: Kaufman, Daniel L.
 ATTORNEY/AGENT INFORMATION:
 ALBRITTON, Allan J
 ERLANDER, Mark G
 TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco

LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-483-952A-31

Query Match 53.6%; Score 67; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 GMAALPRLAFTSE 14
 Db 7 GMAALPRLAFTSE 20

RESULT 7
 US-08-159-339A-933
 Sequence 933, Application US/08159339A
 Patent No. 6037135

GENERAL INFORMATION:
 APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban

TITLE OF INVENTION: HLA Binding peptides and their
 TITLE INVENTION: Uses
 NUMBER OF SEQUENCES: 1234

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 018623-005030US

TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELLEX:

INFORMATION FOR SEQ ID NO: 933:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-159-339A-933

Query Match 32.0%; Score 40; DB 3; Length 10;
 Best Local Similarity 70.0%; Pred. No. 0.6e-06;
 Matches 7; Conservative 2; Mismatches 1; Indels 0;
 Gaps 0;

Qy 12 TSEHSHFSLK 21
 Db 1 TSEQHSYHSIK 10

RESULT 8
 5475086-14
 ; Patent No. 5475086
 ; APPLICANT: TOBIN, ALLAN J.; ERLANDER, MARK G.; KAUFMAN,
 ; DANIEL L.; CLARE-SALZLER, MICHAEL J.
 ; TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
 ; PEPTIDES
 ; NUMBER OF SEQUENCES: 14
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/135,849
 ; FILING DATE: 13-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 716,909
 ; FILING DATE: 18-JUN-1991
 ; APPLICATION NUMBER: 586,536
 ; FILING DATE: 21-SEP-1990
 ; SEQ ID NO:14:
 ; LENGTH: 8
 5475086-14

RESULT 9
 US-08-485-718-2
 Sequence 2, Application US/08485718
 Patent No. 5705626

GENERAL INFORMATION:
 APPLICANT: Tobin, Allan J.
 APPLICANT: ERLANDER, Mark G.
 APPLICANT: KAUFMAN, Daniel L.

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Rohnbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,718
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A60780-6/BIR

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEX: 415-398-3449
 FAX: 415-398-3449

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid

; TOPOLogy: linear
 ; MOLECULE TYPE: protein
 US-08-485-718-2

Query Match 31.2%; Score 39; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6; 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 GMAALPRL 8	Db	17 GMAALPRL 24
RESULT 10	US-08-484530-2	GENERAL INFORMATION:	COMPUTER READABLE FORM:
SEQUENCE 2, Application US/08484530	PATENT NO. 5846740	COMPUTER: IBM PC compatible	
PATENT NO. 5846740	OPERATING SYSTEM: PC-DOS/MS-DOS		
APPLICANT: Erlander, Mark G	SOFTWARE: Patentin Release #1.0, Version #1.30		
APPLICANT: Kaufman, Daniel L.	CURRENT APPLICATION DATA:		
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase	APPLICATION NUMBER: US-08-827,618A		
NUMBER OF SEQUENCES: 60	FILING DATE: 09-ARR-1997		
NUMBER OF SEQUENCES: 60	CLASSIFICATION: 435		
CORRESPONDENCE ADDRESS:	PRIOR APPLICATION DATA:		
ADRESSEE: Flehr, Hohbach, Test, Albritton & Herbert	APPLICATION NUMBER: US 08/485,725		
STREET: Four Embarcadero Center, Suite 3400	FILING DATE: 07-JUN-1995		
CITY: San Francisco	PRIOR APPLICATION DATA:		
STATE: CA	APPLICATION NUMBER: US 07/716,909		
ZIP: 94111-4187	FILING DATE: 18-JUN-1991		
COMPILER READABLE FORM:	PRIOR APPLICATION DATA:		
MEDIUM TYPE: Floppy disk	APPLICATION NUMBER: US 07/586,530		
COMPUTER: IBM PC compatible	FILING DATE: 21-SEP-1990		
OPERATING SYSTEM: PC-DOS/MS-DOS	ATTORNEY/AGENT INFORMATION:		
SOFTWARE: Patentin Release #1.0, Version #1.30	NAME: Ficcartin, Richard F.		
CURRENT APPLICATION DATA:	REGISTRATION NUMBER: 31,801		
APPLICATION NUMBER: US-08-484,530	REFERENCE DOCKET NUMBER: A-60780-12/RFT/MTK		
FILING DATE: 07-JUN-1995	TELECOMMUNICATION INFORMATION:		
CLASSIFICATION: 435	TELEPHONE: 415-781-1989		
ATTORNEY/AGENT INFORMATION:	TELEFAX: 415-398-3249		
NAME: Ficcartin, Richard F.	INFORMATION FOR SEQ ID NO: 2:		
REGISTRATION NUMBER: 31,801	SEQUENCE CHARACTERISTICS:		
REFERENCE DOCKET NUMBER: A-60780-8/RFT/MTK	LENGTH: 24 amino acids		
TELECOMMUNICATION INFORMATION:	TYPE: amino acid		
TELEPHONE: 415-781-1989	STRANDEDNESS: single		
TELEFAX: 415-398-3249	TOPOLogy: linear		
INFORMATION FOR SEQ ID NO: 2:	MOLECULE TYPE: protein		
SEQUENCE CHARACTERISTICS:	US-08-827-618A-2		
LENGTH: 24 amino acids	Query Match 31.2%; Score 39; DB 2; Length 24;		
TYPE: amino acid	Best Local Similarity 100.0%; Pred. No. 2.6; 0; Mismatches 0; Indels 0; Gaps 0;		
STRANDEDNESS: single	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
TOPOLogy: linear	RESULT 12		
MOLECULE TYPE: protein	US-08-483-952A-2		
US-08-484-530-2	SEQUENCE 2, Application US/08483952A		
Query Match 31.2%; Score 39; DB 2; Length 24;	PATENT NO. 6011139		
Best Local Similarity 100.0%; Pred. No. 2.6; 0; Mismatches 0; Indels 0; Gaps 0;	GENERAL INFORMATION:		
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	APPLICANT: Tobin, Allan J		
APPLICANT: Erlander, Mark G	APPLICANT: Kaufman, Daniel L.		
APPLICANT: Kaufman, Daniel L.	TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase		
APPLICANT: Kaufman, Daniel L.	NUMBER OF SEQUENCES: 60		
APPLICANT: Kaufman, Daniel L.	CORRESPONDENCE ADDRESS:		
APPLICANT: Kaufman, Daniel L.	ADRESSEE: Flehr, Hohbach, Test, Albritton & Herbert		
APPLICANT: Kaufman, Daniel L.	STREET: Four Embarcadero Center, Suite 3400		
APPLICANT: Kaufman, Daniel L.	CITY: San Francisco		
APPLICANT: Kaufman, Daniel L.	STATE: CA		
APPLICANT: Kaufman, Daniel L.	COUNTRY: US		
APPLICANT: Kaufman, Daniel L.	ZIP: 94111-4187		
APPLICANT: Kaufman, Daniel L.	COMPUTER READABLE FORM:		

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,952A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,859
 FILING DATE: 17-SEP-1993
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/716,909
 FILING DATE: 18-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
 TELEPHONE: 415-751-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-483-952A-2

Query Match 31.2%; Score 39; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0;
 Gaps 0;
 Qy 1 GMAALPRL 8
 Db 17 GMAALPRL 24

RESULT 13 US-08-282-758B-2
 Sequence 2, Application US/08282758B
 ; Patent No. 5670310
 GENERAL INFORMATION:
 APPLICANT: Fields, Howard A.
 APPLICANT: Khudyakov, Yury E.
 TITLE OF INVENTION: Methods and Compositions for
 Differential Diagnosis of Chronic and Acute Hepatitis C
 TITLE OF INVENTION: Virus Infection
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 ZIP: 30303
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/282,758B
 FILING DATE: 29-JUN-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Green, Jamie L.
 REGISTRATION NUMBER: 32,467
 REFERENCE/DOCKET NUMBER: 03063-0100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 818-3700
 TELEFAX: (404) 818-3799
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-282-758B-2

Query Match 29.6%; Score 37; DB 1; Length 20;
 Best Local Similarity 61.5%; Pred. No. 4.6;
 Matches 8; Conservative 1; Mismatches 4;
 Gaps 0;
 Qy 7 RLIAFTSEHSHFS 19
 Db 3 RLIAFAASGRNHY 15

RESULT 14 PCT-US92-07865-3
 Sequence 3, Application PC/TUUS9207865
 GENERAL INFORMATION:
 APPLICANT: Dreesman, Gordon R.
 APPLICANT: Burk, Kenneth H.
 APPLICANT: Pauletti, Daniel
 TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Law Offices of Peter Dehlinder
 STREET: 350 Cambridge Avenue, Suite 300
 CITY: Palo Alto
 STATE: CA
 COUNTY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/07865
 FILING DATE: 19920916
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 FILING DATE: 16-SEP-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 1600-0086.41
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: AMINO ACID
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Hepatitis C Virus
 INDIVIDUAL ISOLATE: DP3, amino acids 1917 to 1940 of the
 HCV polyprotein
 PCT-US92-07865-3

RESULT 15

Query Match 29.6%; Score 37; DB 5; Length 24;
 Best Local Similarity 61.5%; Pred. No. 5.8; 1; Mismatches 4; Indels 0; Gaps 0;
 Matches 8; Conservative

Qy 7 RLIAFTSBSHES 19
 Db 2 RLIAFASRGHNHVS 14

RESULT 16

US-08-159-339A-915
 Sequence 915, Application US/08159339A

PATENT INFORMATION:

APPLICANT: Kubo, Ralph T.

APPLICANT: Sette, Alessandro

APPLICANT: Grey, Howard M.

APPLICANT: Sette, Alessandro

APPLICANT: Celis, Esteban

TITLE OF INVENTION: HLA Binding peptides and Their

TITLE OF INVENTION: Uses

NUMBER OF SEQUENCES: 1254

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159-339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

RESULT 17

US-08-159-339A-978

Sequence 978, Application US/08159339A

PATENT NO. 6037135

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.

RESULT 17

US-08-159-339A-915

Sequence 915, Application US/08159339A

PATENT NO. 6037135

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.

RESULT 17

US-08-159-339A-915

Sequence 915, Application US/08159339A

PATENT NO. 6037135

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and Their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:
 STREET: Townsend and Townsend and Crew LLP
 CITY: Two Embarcadero Center, Eighth Floor
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastaSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 06-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 018623-0050300US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX:
 INFORMATION FOR SEQ ID NO: 978:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-159-339A-978

RESULT 18
 Query Match 27.2%; Score 34; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred No. 1.6e+05;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TAFTSHH 17
 : ||| | |
 Db 1 VLFTEQSH 9

RESULT 18
 Query Match 27.2%; Score 34; DB 2; Length 22;
 Best Local Similarity 63.6%; Pred No. 1.7e+05;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 RLIATPSESH 17
 : ||| | | | | |
 Db 11 RLIATPASRGNH 21

RESULT 19
 US-08-723-425A-58
 Sequence 58, Application US/08723425A
 Patent No. 6165730

GENERAL INFORMATION:
 APPLICANT: ROBERT
 DELLEYS,
 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
 PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
 EPITOPE AND THEIR USE IN A PROCESS FOR DETERMINATION OF
 EPITOPE AND THEIR USE IN A PROCESS FOR DETERMINATION OF
 PEPTIDES CORRESPONDING . . .
 TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING . . .
 NUMBER OF SEQUENCES: 453
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE, P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: Arlington
 STATE: VA
 COUNTRY: USA
 ZIP: 22201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/723,425A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B.J.
 REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 14,487-13
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-816-4000
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: HCV
 FEATURE:

NAME/KEY: Modified-site
LOCATION: 1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 22
US-08-723-425A-58

Query Match 27.2%; Score 34; DB 4; Length 22;
Best Local Similarity 63.6%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 20
US-09-112-206-58
Sequence 58, Application US/09112206
Patient No. 610903
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPE AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPE,
TITLE OF INVENTION: PROCESSES FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/112,206
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536.
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-6/BIR

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-338-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide

US-08-485-718-1

RESULT 22
Query Match 26.4%; Score 33; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 27; Mismatches 2; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match 26.4%; Score 33; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 27; Mismatches 2; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 22
Query Match 26.4%; Score 33; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 27; Mismatches 2; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match 27.2%; Score 34; DB 4; Length 22;
Best Local Similarity 63.6%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 21
US-08-485-718-1
Sequence 1, Application US/08485718
Patient No. 570526
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.

APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
ZIP: 94111-1187
COUNTRY: US

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 INFORMATION FOR SEQ ID NO: 1:
 LENGTH: 23 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-484-530-1

Query Match 26.4%; Score 33; DB 2; Length 23;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMAALPRL 8
 Db 16 GMAAVPKL 23

RESULT 24
 US-08-483-952A-1

Sequence 1, Application US/08483952A
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Tobin, Allan J
 ; APPLICANT: Erlander, Mark G
 ; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,952A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/123,859
 ; FILING DATE: 17-SEP-1993
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION NUMBER: US 07/586,536
 ; FILING DATE: 18-JUN-1991
 ; CLASSIFICATION: 536
 ; PRIORITY/AGENT INFORMATION:
 ; NAME: Trecartin, Richard F.
 ; REGISTRATION NUMBER: 31,801
 ; REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 23 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-483-952A-1

Query Match 26.4%; Score 33; DB 3; Length 23;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMAALPRL 8
 Db 16 GMAAVPKL 23

Db ||||:||
16 GMAAVPKL 23

RESULT 25

5475086-8

PATENT NO. 5475086
APPLICANT: TOBIN, ALLAN J.; ERLANDER, MARK G.; KAUFMAN,
DANIEL L.; CLARE SALZIER, MICHAEL J.

TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE

PEPTIDES

NUMBER OF SEQUENCES: 14

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/135,849

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 716,909

FILING DATE: 18-JUN-1991

APPLICATION NUMBER: 586,536

FILING DATE: 21-SEP-1990

SEQ ID NO:8;

LENGTH: 24

5475086-8

Query Match 26.4%; Score 33; DB 6; Length 24;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRL 8

Db ||||:||
17 GMAAVPKL 24

Search completed: January 6, 2002, 09:52:30
Job time: 226 sec

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 6, 2002, 09:49:29 ; Search time 19.62 Seconds
 (without alignments)
 97.062 Million cell updates/sec

Sequence: US-09-441-061-2

Scoring table: BLOSUM62

Gap_p 10.0 , Gapext. 0.5

Searched: 219241 seqs, 7617452 residues

Total number of hits satisfying chosen parameters: 4959

Minimum DB seq length: 0

Maximum DB seq.length: 25

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 50 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	32	25.6	2 H64710	hypothetical protein H64710
2	29	23.2	2 S03949	hypothetical protein Hp1528 - Helicobacter pylori (strain 26695)
3	27	21.6	14 2 PS0449	C;Species: Helicobacter pylori
4	26	20.8	10 2 PC2171	C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
5	26	20.8	22 2 B39138	C;Accession: H64710 R;From: J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, J. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Kusalik, H.G.; Glodek, A.; McKesson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 308, 539-547, 1987
6	26	20.8	24 2 I73619	A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
7	25	20.0	8 XGHOED	A;Reference number: A64520; MUID:97394467
8	25	20.0	22 2 A28563	A;Accession: H64710
9	24.5	19.6	20 2 S07232	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
10	24	19.2	20 2 A53875	A;Molecule type: DNA
11	24	19.2	22 2 S40638	A;Residues: 1-25 <DTR>
12	24	19.2	22 2 F84018	A;Cross-references: GB:AB000651; GB:AE000511; NID:92314708; PIDN:AAD08577.1; PID:92314708
13	24	19.2	25 2 J00361	RESULT 2
14	23	18.4	14 2 A60770	hypothetical protein H64710
15	23	18.4	15 2 PS0455	N;Alternate names: alpha-endothelial cell growth factor
16	23	18.4	15 2 PT0094	C;Species: Sus scrofa domesticus (domestic pig)
17	23	18.4	15 2 S66627	C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
18	23	18.4	22 2 A17267	C;Accession: S03954 R;Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Iuethe, N.; Sharma, H.S.; Sc
19	23	18.4	22 2 R86453	Eur.; J. Biochem. 181, 67-73, 1989
20	23	18.4	23 2 PH0853	A;Title: Isolation of heparin-binding growth factors from bovine, porcine and canine Maud Protein - Par
21	23	18.4	24 2 A36912	A;Reference number: S03953; MUID:89231704
22	23	18.4	24 4 S09363	A;Accession: S03954
23	22	17.6	10 2 S4176	A;Molecule type: protein
24	22	17.6	12 2 S01122	A;Residues: 1-20 <QUR>
25	22	17.6	12 2 PH1535	C;Keywords: growth factor
26	22	17.6	13 2 B61620	
27	22	17.6	15 2 PA0087	
28	22	17.6	16 2 A85822	
29	22	17.6	18 2 S48862	

ALIGNMENTS

Query	Match	Score	DB	Length
1	23.28	29	DB 2	Length 20;

Best Local Similarity 35.7%; Pred. No. 3e+02; 3; Mismatches 6; Indels 0; Gaps 0;

Qy 5 LPRLI AFTSEHSHF 18
| | ; : | |
Db 3 LPPKLYSSNGHF 16

RESULT 3
porin - rice' (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0249
R;Tsugita, A.
submitted to JIBID, April 1993
A;Reference number: PS0206
A;Accession: PS0249
A;Molecule type: Protein
A;Residues: 1-14 <res>
A;Experimental source: callus

Query Match Score 27; DB 2; Length 14;
Best Local Similarity 30.8%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 9 IAFTSEHSHFSTK 21
: | | ; : |
Db 2 VTFDDHTANGIK 14

RESULT 4
PC2171 triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fragment)
C;Species: Rhizopus niveus
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: PC2171
R;Kohno, M.; Kugimura, W.; Hashimoto, Y.; Morita, Y.
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994
A;Title: Purification, characterization, and crystallization of two types of lipase from
A;Reference number: PC2171; MUID:94319059
A;Accession: PC2171
A;Molecule type: protein
A;Residues: 1-10 <KOH>
C;Comment: this enzyme catalyzes the hydrolysis of the ester bonds.
C;Keywords: carboxylic ester hydrolase

Query Match Score 26; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AAALPRLIA 10
Db 3 AAALPPLIS 10

RESULT 5
B39138 dihydroliopamide S-acetyltransferase (EC 2.3.1.12) - Pelobacter carbinolicus (fragment)
C;Species: Pelobacter carbinolicus
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 05-May-2000
C;Accession: B39138
R;Oppermann, F.B.; Schmidt, B.; Steinbüchel, A.
J. Bacteriol. 173, 757-767, 1991
A;Title: Purification and characterization of acetoin:2,6-dichlorophenolindophenol oxidase acetoate dehydrogenase enzyme system.
A;Reference number: A39138; MUID:911003666
A;Accession: B39138
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <OPO>

C;Superfamily: dihydroliopamide acetyltransferase; lipoyl/biotin-binding homology
C;Keywords: acyltransferase; coenzyme A

Query Match Score 26; DB 2; Length 22;
Best Local Similarity 29.4%; Pred. No. 1e+03;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 RLIAFTSEHSHSLSLKKG 23
| : | | ; : : |
Db 4 RILALTMPKKGLTMEEG 20

RESULT 6
IT73619 endothelial growth factor receptors fit [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: IT73619
R;Bocock, C.A.; Charnock-Jones, D.S.; Sharkey, A.M.; McLaren, J.; Barker, P.J.; WR
J. Natl. Cancer Inst. 87, 506-516, 1995
A;Title: Expression of vascular endothelial growth factor and its receptors fit and
A;Reference number: 156493; MUID:9522657
A;Accession: IT73619
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-24 <res>
A;Cross-references: GB:S77814; NID:9998566; PIDN:AAB34002.1; PID:9998567
C;Genetics:
A;Gene: fit

Query Match Score 26; DB 2; Length 24;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 ATFTSEHSHF 18
| : | : |
Db 14 SFSSNYFHF 22

RESULT 7
XGHHEU urine glycopeptide - human
C;Species: Homo sapiens (man)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A03188
R;Loe, C.J.; Weiss, J.B.
Biochem. J. 123, 25P, 1971
A;Title: Identification in urine of a low-molecular-weight polar glycopeptide conta
A;Reference number: A03188; MUID:72062338
A;Accession: A03188
A;Molecule type: protein
A;Residues: 1-8 <res>
C;Comment: The identity of the glycoprotein from which this peptide is derived is u
re has also been found (see PIR:XHUE).
C;Keywords: glycoprotein
F;1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match Score 25; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 EHSH 17
| | | |
Db 2 EHSH 5

RESULT 8
A28563 hemoglobin chain III - earthworm (Lumbricus terrestris) (fragment)

C;Species: Lumbricus terrestris (common earthworm)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 04-Mar-2000
C;Accession: A28563
R;Gotoh, T.; Shishikura, F.; Snow, J.W.; Erefej, K.I.; Vinogradov, S.N.; Walz, D.A.
BIOCHEM. J. 241, 441-445, 1987
A;Title: Two globin strains in the giant annelid extracellular haemoglobins.
A;Reference number: A00337; MUID:87241210
A;Accession: A28563
A;Residues: 1-22 <GOT>
C;Superfamily: globin; globin homology
C;Keywords: oxygen carrier

RESULT 9
S07232 Query Match 20.0%; Score 25; DB 2; Length 22;
ribulose-bisphosphate carboxylase subunit-binding protein alpha chain (frag)
N;Alternate names: rubisco subunit-binding protein alpha chain
C;Species: Pisum sativum (garden pea)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C;Accession: S07232
R;Mugrove, J.E.; Johnson, R.A.; Ellis, R.J.
Eur. J. Biochem. 163, 529-534, 1987
A;Title: Dissociation of the ribulosebisphosphate-carboxylase large-subunit binding prot
A;Reference number: S07232; MUID:87161853
A;Accession: S07232
A;Molecule type: protein
A;Residues: 1-20 <HUS>
C;Comment: This protein binds the newly synthesized large subunit and the newly imported
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Query Match 19.6%; Score 24.5; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.6e+03; Matches 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 IAFSEHSFSLSKG 23
||| :|| ::|
Db 5 IAF-DQHRSAMOG 18

RESULT 10
A53875 Query Match 19.2%; Score 24; DB 2; Length 22;
creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)
C;Species: Oncorhynchus kisutch (coho salmon)
C;Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997
C;Accession: A53875
R;White, K.C.; Babitt, P.C.; Buechter, D.D.; Kenyon, G.L.
J. Protein Chem. 11, 480-494, 1992
A;Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB 1s
A;Reference number: A53875; MUID:93080727
A;Accession: A53875
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-20 <WII>
A;Experimental source: Brockmann body, principal islet
A;Note: sequence extracted from NCBI backbone (NCBIP:120599)
C;Superfamily: creatine kinase; creatine kinase repeat homology
C;Keywords: phosphotransferase

Query Match 19.2%; Score 24; DB 2; Length 20;

RESULT 11
Oy 11 FTSESHFSL 20
|| :|| |
Db 2 FGNTHRNFKL 11

Query Match 20.0%; Score 25; DB 2; Length 22;
Best Local Similarity 40.0%; Pred. No. 1.9e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 13 SEISHFSIKK 22
||| :|| |
Db 8 SEBDHYIVOK 17

RESULT 12
S40638 Query Match 19.2%; Score 24; DB 2; Length 22;
ATP-43 protein - human (fragments)
C;Species: Homo sapiens (man)
C;Accession: S40638
R;Hurst, H.C.; Totty, N.F.; Jones, N.C.
Nucleic Acids Res. 19, 4601-4609, 1991
A;Title: Identification and functional characterisation of the cellular activating t.
A;Reference number: S40638; MUID:91367654
A;Accession: S40638
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <HUR>

Query Match 19.2%; Score 24; DB 2; Length 22;
Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 ALPRLIAFTS 13
||| :|| :|| |
Db 13 SLPQTVVMTS 22

RESULT 13
F84018 Query Match 19.2%; Score 24; DB 2; Length 22;
hypothetical protein BH2950 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: F84018
R;Takami, H.; Nakase, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliiphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20263314
A;Accession: F84018
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <STO>
A;Cross-references: GB:AP001517; GB:BA000004; NID:910175500; PIDN:BAB06669.1; GSPDB:
A;Genetics:
A;Gene: BH2950

Query Match 19.2%; Score 24; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSLKKG 23
||| :|| |
Db 8 FSLEKG 13

RESULT 14
JO0361 Query Match 19.2%; Score 24; DB 2; Length 22;
vasoactive intestinal peptide - Atlantic cod (fragment)
C;Species: Gadus morhua (Atlantic cod)
C;Accession: JO0361
R;Twaijles, D.T.; Young, J.; Thorndyke, M.C.; Dimaline, R.
Regul. Pept. 21, 436, 1988
A;Title: Isolation and characterisation of two teleost VIP's.
A;Reference number: JO0361

Query Match 19.2%; Score 24; DB 2; Length 20;

A; Molecule type: protein
 A; Residues: 1-25 <PRW>
 C; Superfamily: glucagon
 C; Keywords: duplication; intestine; neuropeptide

Query Match Score 24; DB 2; Length 25;
 Best Local Similarity 35.7%; Pred. No. 2.4e+03;
 Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 11 FTSEHSHFSKKGA 24
 DB 6 FTDNYSRFRKOMAA 19

RESULT 14

A60770 cell surface alloantigen gp60 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: A60770 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-Feb-1997
 R; Schadendorf, D.; Yamaguchi, H.; Old, L.J.; Srivastava, P. K.
 A;Title: A novel heteromorphic human cell surface alloantigen, gp60, defined by a human
 A;Reference number: A60770; MUID:89140352
 A;Accession: A60770
 A;Molecule type: protein
 A;Residues: 1-14 <SCH>
 C;Comment: This protein is an alloantigen in human populations but is not found on cells
 C;Comment: This protein exists in both membrane bound and cytosolic forms.
 C;Keywords: glycoprotein; polymorphism; surface antigen

Query Match Score 23; DB 2; Length 14;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 TAFTSEHSHF 18
 DB 5 VSFTXESXGF 14

RESULT 15

PS0455 superoxide dismutase (EC 1.15.1.1) (Mn) - rice (strain Nipponbare) (fragment)
 C;Species: Oriza sativa (rice)
 C;Accession: PS0455
 R;Tsugita, A.
 submitted to JIPID, April 1993
 A;Reference number: PS0206
 A;Accession: PS0455
 A;Molecule type: protein
 A;Residues: 1-15 <TSU>
 A;Experimental source: germ
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Keywords: metalloprotein; oxidoreductase

Query Match Score 23; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GNAALPHL 8
 DB 2 GIVALPL 9

RESULT 16

PR0094 succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) 27k iron-sulfur protein, mitochondrial
 C;Species: Mus musculus (house mouse)

RESULT 19
 H86433 Protein T17W7.9 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision: 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: H86433
 R;Residues: 1-24 <FRA>
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C.;
 C.R.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Salano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719
 A;Accession: H86433
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-22 <STO>
 A;Cross-references: GB:AE005172; NID:94926824; PIDN:AD32934.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: T17W7.9
 A;Map position: 1

RESULT 20
 PH0588 Query Match 18.4%; Score 23; DB 2; Length 22;
 Best Local Similarity 62.5%; Pred No. 3.1e+03; Mismatches 5; Conservative 1; Indels 0; Gaps 0;
 Matches 5; Mismatches 2; Indels 0; Gaps 0;
 QY 13 SERSHFSL 20.
 ||| :|||
 Db. 13 SERNEFSL 20

RESULT 20
 PH0588 Query Match 18.4%; Score 23; DB 2; Length 22;
 Best Local Similarity 62.5%; Pred No. 3.1e+03; Mismatches 5; Conservative 1; Indels 0; Gaps 0;
 Matches 5; Mismatches 2; Indels 0; Gaps 0;
 QY 13 SERSHFSL 20.
 ||| :|||
 Db. 13 SERNEFSL 20

RESULT 20
 PH0588 Maud protein - *Paracoccus denitrificans* (fragment)
 C;Species: *Paracoccus denitrificans*
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
 C;Accession: PH0588
 R;Chistosoerov, A.Y.; Boyd, J.; Mathews, F.S.; Lidstrom, M.E.
Biochem. Biophys. Res. Commun. 184, 1181-1189, 1992
 A;Title: The genetic organization of the mau gene cluster of the facultative autotroph *P. denitrificans*.
 A;Reference number: PH0586; MUID:9227206
 A;Accession: PH0588
 A;Molecule type: DNA
 A;Residues: 1-23 <CHI>
 A;Cross-references: GB:M90098; NID:9150580; PIDN:AAA25577.1; PID:9150581
 A;Genetics:
 A;Gene: mauD

RESULT 23
 S74176 Query Match 18.4%; Score 23; DB 4; Length 24;
 Best Local Similarity 36.0%; Pred. No. 3.2e+03; Mismatches 4; Conservative 3; Indels 8; Gaps 1;
 Matches 9; Mismatches 5; Indels 8; Gaps 1;
 QY 17 HFSIKK 22
 ||| :||| :|||
 Db. 7 HFSTOK 12

RESULT 23
 S74176 Query Match 18.4%; Score 23; DB 4; Length 24;
 Best Local Similarity 36.0%; Pred. No. 3.2e+03; Mismatches 4; Conservative 3; Indels 8; Gaps 1;
 Matches 9; Mismatches 5; Indels 8; Gaps 1;
 QY 17 HFSIKK 22
 ||| :||| :|||
 Db. 7 HFSTOK 12

RESULT 21
 A36912 Hypothetical protein 1 batG-region [imported] - *Eubacterium* sp. (fragment)
 C;Species: *Eubacterium* sp.
 C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C;Accession: A36912
 R;Franklund, C.V.; Baron, S.F.; Hylemon, P.B.
J. Bacteriol. 175, 3002-3012, 1993
 A;Title: Characterization of the batG gene encoding a bile acid-inducible NADH:flavin ox
 A;Reference number: A36912; MUID:93259945

RESULT 22
 A;Accession: A96912
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-24 <FRA>
 A;Experimental source: VPI 12708
 A;Note: sequence extracted from NCBI backbone (NCIN:131883, NCIBP:131906)
 Query Match 18.4%; Score 23; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03; Mismatches 5; Conservative 2; Indels 3; Gaps 0;
 Matches 5; Mismatches 3; Indels 0; Gaps 0;
 QY 5 LPRLIAFSE 14
 ||| | :|||
 Db. 4 LPVLILFLQ 13

RESULT 22
 S09363 Query Match 18.4%; Score 23; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03; Mismatches 5; Conservative 2; Indels 3; Gaps 0;
 Matches 5; Mismatches 3; Indels 0; Gaps 0;
 A;Accession: S09363
 A;Molecule type: DNA
 A;Residues: 1-24 <POU>
 A;Cross-references: This is the hypothetical translation of a sequence believed to result from
 C;Genetics:
 A;Gene: MTCO1/MTCYB
 A;Genome: mitochondrial
 A;Genetic code: SG31
 C;Keywords: fusion protein; mitochondrial F1-ATPase; cytochrome-c oxidase chain I
 F1-ATPase; Region: cytochrome b (+2 frame shifted)

RESULT 23
 S74176 Query Match 18.4%; Score 23; DB 4; Length 24;
 Best Local Similarity 66.7%; Pred. No. 3.4e+03; Mismatches 4; Conservative 1; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Indels 0; Gaps 0;
 QY 17 HFSIKK 22
 ||| :|||
 Db. 7 HFSTOK 12

RESULT 23
 S74176 Query Match 17.6%; Score 22; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 3; Conservative 1; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Indels 0; Gaps 0;

QY 12 TSERSH 17

Db 1: | |
 2 TTNNDH 7

RESULT 24

S01122
Photosystem II 3.7K protein - spinach (fragment)
C;Species: Spinacia olaracea (spinach)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: S01122
R;Schroeder W.P.; Hentysson, T.; Akerlund, H.E.
FEBS Lett. 235, 289-292, 1988
A;Title: Characterization of low molecular mass proteins of photosystem II by N-terminal
A;Reference number: S01120
A;Accession: S01122
A;Molecule type: protein
A;Residues: 1-12 <SCH>
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
QY	5 LPRLIAFS 13	17.6%	22	DB 2;	Length 12;			
Matches	5; Conservative	55.6%	Pred. No. 2.4e+03;		0;	0;	0;	0;
Db	2 LPEAYAFLS 10							

RESULT 25

PH1635
Ig H chain V-D-J region (clone B-less 218) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1635
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609
A;Accession: PH1635
A;Molecule type: DNA
A;Residues: 1-12 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
QY	3 AALPRLIAF 11	17.6%	22	DB 2;	Length 12;			
Matches	3; Conservative	44.4%	Pred. No. 2.4e+03;		2;	0;	0;	0;
Db	2 AGLPGGLCY 10							

Search completed January 6, 2002, 09:53:18
Job time: 229 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: January 6, 2002, 09:52:34 ; Search time 12.98 Seconds
(without alignments)

Sequence: US-09-441-061-2
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Title: Perfect score: 125
Sequence: 1 GMAALPRLIAFTSEHSHFSLKKGAA 25

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Maximum Match 0%

Listing first 50 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	28.5	MISG_MISAN	21	1	P81474	misgurnus a
2	22.8	CRL1_LITSP	25	1	P56226	litoria spl
3	20.8	CRL2_LITCE	25	1	P56227	litoria cae
4	20.8	CRL3_LITCE	25	1	P56228	litoria cae
5	20.8	CRL4_LITGI	25	1	P56229	litoria gil
6	20.0	GLUR_HUMAN	8	1	P02729	homo sapien
7	20.0	FRE4_LITIN	24	1	P82023	litoria inf
8	19.2	CRL5_LITCE	25	1	P56230	litoria cae
9	19.2	VIP_GDRM	12	1	P81555	periplaneta
10	18.4	PVFL_PERAM	22	1	P19069	cavia porce
11	18.4	CO4_CAVPO	23	1	P29134	thlobacillus
12	18.0	CH00_THIFE	13	1	P41490	locusta mig
13	17.6	LMFL_LOM1	18	1	P01458	muss musculus
14	17.6	CYCH_MOUSE	21	1	P43171	escaris suu
15	16.8	RART_ASCSU	16	1	P03058	escherichia
16	16.8	LPHL_ECOLI	22	1	P33027	salmonella
17	16.8	SETB_SALTY	21	1	P80400	ana rugosa
18	16.8	GABE_RANRU	24	1	P82152	cycla pompon
19	16.0	ALLI_CYDPO	8	1	P02728	homo sapien
20	16.0	GLEM_HUMAN	10	1	P04378	petromyzon
21	16.0	GONI_PETMA	15	1	P82648	lactobacilli
22	16.0	ASPL_LACSN	15	1	P56226;	rhodococcus
23	16.0	MCA2_RHOOP	20	1	P07448	rattus norv
24	16.0	DFPS_RAT	20	1	P05658	bacillus st
25	16.0	LPTR_BACST	20	1	P33404	trichomonas
26	16.0	CYSP_TRIVIA	22	1	P45440	streptomyce
27	16.0	LPER_STRIER	24	1	P09124	lactococcus
28	16.0	SCRK_LACTIA	25	1	P80447	lactic acid
29	15.6	G3P2_JACOR	19	1	P37041	alligator m
30	15.2	GONI_ALLMI	10	1	P56639	conus aulic
31	15.2	CXAL_CONNL	16	1	P81816	carcinis ma
32	15.2	AL3_CARMA	18	1	P99504	canis famili
33	15.2	ATPB_CANFIA	19	1		

ALIGNMENTS

SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1 AND 1.1.2.

RESULT 1
ID MMSG_MISAN
Description P81474;
STANDARD; PRT; 21 AA.
AC P81474;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MISGURNIN.
OS Misgurnus anguillicaudatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cobitidae; Misgurnus.
OX NCBI-TaxID=75329;
RN [1]-7502 NW; 4A6E9D0AB391BCF1 CRC64;

RX MEDLINE-9715401; PubMed-9271200;
RA Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.;
RT "A novel antimicrobial peptide from the loach, Misgurnus anguillicaudatus";
RT FEBS Lett. 411:173-178(1997).
CC - FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA AND FUNGI.
CC - MASS SPECTROMETRY: MW=2502; METHOD-MALDI.
KW Antimicrob; fungicide.
SQ SEQUENCE 21 AA; 2502 NW; 4A6E9D0AB391BCF1 CRC64;

Query Match Best Local Similarity 75.0%; Pred. No. 1.9e-02; Length 21; Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1; OQ 14 EHSHRSLLKKGA 25
Db 6 BLSKFS-KKGAA 16

RESULT 2
ID CR11_LITSP
STANDARD; PRT; 25 AA.
AC P56226;
DT 15-JUL-1998 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERN 1.1.
OS litoria splendida, Litoria gilleni, and Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
OC litoria.
OX NCBI-TaxID=30345, 39405, 30344;
RN [1]
RP

RC SPECIES="L.spandida"; TISSUE="Parotoid gland";
 RA Stone D.J.M.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
 RT "Peptides from Australian frogs. Structures of the caerins and
 caeridin 1 from *Litoria splendida*.";
 RL J. Chem. Soc. Parkin Trans. 1:3173-3178(1992).
 RN [2]
 RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1; 1.1.2 AND 1.1.4.
 RC SPECIES="L.caerulea; TISSUE=Parotoid gland";
 RA Stone D.J.M.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea."
 RL J. Chem. Res. 138:937-961(1993).
 RN [3]
 RP SEQUENCE, AND MASS SPECTROMETRY OF 1.1; 1.1.1; 1.1.3; 1.1.5 TO 1.1.8.
 RC SPECIES="L.gilleni"; TISSUE=Parotoid gland; Peptide ID: 92666696;
 RA Wong H.; Bowie J.H.; Carver J.A.;
 RT "The solution structure and activity of caerin 1.1, an antimicrobial
 peptide from the Australian green tree frog, *Litoria splendida*,";
 RL Eur. J. Biochem. 247:545-557(1997).
 CC -1- PTM: THE MAJOR PRODUCT IS CAERIN 1.1. IN ADDITION, DIFFERENT
 PEPTIDES ARE PRODUCED THAT ARE MISSING SOME AMINO ACID RESIDUES AT
 THE N-TERMINUS OR C-TERMINUS. ALL ISOFORMS ARE NOT REPRESENTED IN
 EACH SPECIES. CAERIN 1.1.1 AND CAERIN 1.1.4 ARE INACTIVE.
 CC -1- MASS SPECTROMETRY: MW=258.2; METHOD=FAB; RANGE=1-55.
 CC -1- MASS SPECTROMETRY: MW=241.2; METHOD=FAB; RANGE=3-35.
 CC -1- MASS SPECTROMETRY: MW=229.9; METHOD=FAB; RANGE=4-25.
 CC -1- MASS SPECTROMETRY: MW=142.1; METHOD=FAB; RANGE=13-25.
 CC -1- MASS SPECTROMETRY: MW=142.1; METHOD=FAB; RANGE=1-33.
 CC -1- MASS SPECTROMETRY: MW=162.6; METHOD=FAB; RANGE=1-16.
 CC -1- MASS SPECTROMETRY: MW=148.9; METHOD=FAB; RANGE=1-15.
 CC -1- MASS SPECTROMETRY: MW=118.0; METHOD=FAB; RANGE=1-12.
 KW Antibiotic; Antiviral; Amphibian skin; Amidation.
 FT PEPTIDE 1 25 CAERIN 1.1.
 FT PEPTIDE 3 25 CAERIN 1.1.1.
 FT PEPTIDE 4 25 CAERIN 1.1.2.
 FT PEPTIDE 13 25 CAERIN 1.1.3.
 FT PEPTIDE 1 23 CAERIN 1.1.4.
 FT PEPTIDE 1 16 CAERIN 1.1.5.
 FT PEPTIDE 1 15 CAERIN 1.1.6.
 FT PEPTIDE 1 12 CAERIN 1.1.7.
 FT PEPTIDE 1 10 CAERIN 1.1.8.
 FT MOD_RES 25 25 AMIDATION.
 SQ SEQUENCE 25 AA; 2585 MW; D8A5AA460BB0EBE00 CRC64;

Query Match Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LPRLIATSEH 15
 | | : | |
 Db 14 LPHVVPVIAEH 24

Query Match Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LPRLIATSEH 15
 | | : | |
 Db 14 LPHVVPVIAEH 24

RESULT 3
 CR12_LITCE STANDARD; PRT; 25 AA.

CC CR13_LITCE STANDARD; PRT; 25 AA.
 AC CR13_LITCE STANDARD; PRT; 25 AA.
 AC P56228;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

RL DECAERIN 1.2.
 OS Litoria caerulea.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
Litoria caerulea."
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTI-BACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY
 SIMILARITY).
 CC -1- MASS SPECTROMETRY: MW=255.2; METHOD=FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 25 25 AMIDATION.
 SQ SEQUENCE 25 AA; 2555 MW; D8A5AA460BB1464C0 CRC64;

Query Match Score 26; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LPRLIATSEH 15
 | | : | |
 Db 14 LPHVVPVIAEH 24

RESULT 3
 CR12_LITCE STANDARD; PRT; 25 AA.

CC CR13_LITCE STANDARD; PRT; 25 AA.
 AC CR13_LITCE STANDARD; PRT; 25 AA.
 AC P56228;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

RL DECAERIN 1.2.
 OS Litoria caerulea.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
Litoria caerulea."
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTI-BACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY
 A REGION OF LESS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY
 SIMILARITY).
 CC -1- MASS SPECTROMETRY: MW=258.2; METHOD=FAB.

QY	5	LPRRIATSEH	15	Score 26; DB 1; Length 25; Best Local Similarity 36.4%; Pred. No. 5.9e+02; Mismatches 4; Indels 0; Gaps 0;	OC NCBL_TaxID=9605; [1]
Db	14	LPNVVPVIAEH	24	RESULT 5 CRA_4_LTRGI ID CRA4_LTRGI STANDARD: PRT; 25 AA. P52229; AC DT 15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) DT 15-JUL-1998 (Rel. 36, Last annotation update) DE CAERIN 1.4. OS Litoria gilleni, and Litoria caerulea. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; OC Litoria. OX NCBI_TaxID=39405, 30344; RN RP SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 1.4. RC SPECIES=L.caerulea; TISSUE=Parotoid gland; RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.; RT "Peptides from Australian frogs. The structures of the caerins and caeridins from Litoria gilleni.", RL J. Chem. Res. 139:937-951(1993). RT "-I - FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY." RT "-I - TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS. CC CC -I - DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY A REGION OF LISS-DEFINED HELICITY AND GREATER FLEXIBILITY (BY SIMILARITY). CC SPCTEST,L.gilleni; TISSUE=Parotoid gland; RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.; RT "Peptides from Australian frogs. The structures of the caerins and caeridins from Litoria gilleni.", RL J. Chem. Res. 139:937-951(1993). RT "-I - FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY." RT "-I - TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS.	OC NCBL_TaxID=9605; [1] SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 1.4. RT glycopeptide containing cysteinyl-galactose. RL Biochem. J. 123:25P-25P(1971). CC -I - FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A SIMILAR STRUCTURE HAS ALSO BEEN FOUND. RA Lotte C.J., Weiss J.B.; CC PIR; A03188; XSGHEU. DR Glycoprotein. FT CARBOHYD 1 1 S-LINED (GAL...) SQ SEQUENCE 8 AA; 855 MW; C2D8TA1F5B1EB1E CRC64;
QY	14	EHSH	17	RESULT 7 FRE4_LITIN ID FRE4_LITIN STANDARD: PRT; 24 AA. P82023; AC DT 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DE FRENTIN 4. OS Litoria infrafrenata (Giant tree frog); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; OC Litoria. OX NCBI_TaxID=61195; RN RP SEQUENCE, AND MASS SPECTROMETRY. RC TISSUE=Skin secretion; RX MEDLINE=9736837; PubMed=9225251; RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.; RT "The structures of the frenatin peptides from the skin secretion of the giant tree frog Litoria infrafrenata.", RL J. Pept. Sci. 2:117-124(1996). CC -I - FUNCTION: WIDE SPECTRUM ANTIMICROBIAL PEPTIDE. CC -I - TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS. CC -I - MASS SPECTROMETRY: MW=2493; METHOD=FAB. SQ SEQUENCE 24 AA; 2495 MW; 6986D063947805A1 CRC64;	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9605; [1] SEQUENCE. MEDLINE=72062338; PubMed=5126885; RA Lotte C.J., Weiss J.B.; RT glycopeptide containing cysteinyl-galactose. RL Biochem. J. 123:25P-25P(1971). CC -I - FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A SIMILAR STRUCTURE HAS ALSO BEEN FOUND. RA Lotte C.J., Weiss J.B.; CC PIR; A03188; XSGHEU. DR Glycoprotein. FT CARBOHYD 1 1 S-LINED (GAL...) SQ SEQUENCE 8 AA; 855 MW; C2D8TA1F5B1EB1E CRC64;
QY	5	LPRRIATSEH	15	Query Match 20.8%; Score 26; DB 1; Length 25; Best Local Similarity 36.4%; Pred. No. 5.9e+02; Mismatches 4; Indels 0; Gaps 0;	OC NCBL_TaxID=9605; [1]
Db	14	LPNVVPVIAEH	24	RESULT 6 GLUR_HUMAN ID GLUR_HUMAN STANDARD: PRT; 8 AA. P02729; AC DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 20-AUG-2001 (Rel. 40, Last annotation update) DE URINE GLUCOPERTE. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC NCBL_TaxID=9605; [1] SEQUENCE. MEDLINE=72062338; PubMed=5126885; RA Lotte C.J., Weiss J.B.; RT glycopeptide containing cysteinyl-galactose. RL Biochem. J. 123:25P-25P(1971). CC -I - FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A SIMILAR STRUCTURE HAS ALSO BEEN FOUND. RA Lotte C.J., Weiss J.B.; CC PIR; A03188; XSGHEU. DR Glycoprotein. FT CARBOHYD 1 1 S-LINED (GAL...) SQ SEQUENCE 8 AA; 855 MW; C2D8TA1F5B1EB1E CRC64;
QY	20	LKKGAA	25	Query Match 20.0%; Score 25; DB 1; Length 24; Best Local Similarity 83.3%; Pred. No. 8.1e+02; Mismatches 5; Conservative 1; Indels 0; Gaps 0;	OC NCBL_TaxID=9605; [1]
Db	6	LKKGAS	11	RESULT 8 CRIS_LTCE ID CRIS_LTCE AC P56230; DT 15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) DT 15-JUL-1998 (Rel. 36, Last annotation update)	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9605; [1] SEQUENCE. MEDLINE=72062338; PubMed=5126885; RA Lotte C.J., Weiss J.B.; RT glycopeptide containing cysteinyl-galactose. RL Biochem. J. 123:25P-25P(1971). CC -I - FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A SIMILAR STRUCTURE HAS ALSO BEEN FOUND. RA Lotte C.J., Weiss J.B.; CC PIR; A03188; XSGHEU. DR Glycoprotein. FT CARBOHYD 1 1 S-LINED (GAL...) SQ SEQUENCE 8 AA; 855 MW; C2D8TA1F5B1EB1E CRC64;

DE CAERIN 1.5.	Best Local Similarity 35.7%; Pred. No. 1.2e+03;
OS Litoria caerulea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OC Eukaryota; Metazoa; Anura; Neobatrachia; Bufonoidea; Hyliidae;	
CC Litoria;	
NCBI_TAXID=30344;	
RN [1]	
RP SOURCE, AND MASS SPECTROMETRY.	
RC TISSUE-Parotoid gland;	
RA Stone D.J.M., Waugh R.J., Bowie J.C., Wallace J.C., Tyler M.J.;	
RT RT Peptides from Australian frogs. The structures of the caerins from	
RT Litoria caerulea.;	
RL J. Chem. Res. 138:910-936(1993).	
CC -1- FUNCTION: ANTI-BACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAPRIN	
CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.	
CC -1- TISSUE-SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS.	
CC -1- DOMAIN: CONTAINS TWO AMPHIPATHIC ALPHA HELIX REGIONS SEPARATED BY A REGION OF LESS-DEFINED HELIX AND GREATER FLEXIBILITY (BY SIMILARITY).	
CC -1- MASS SPECTROMETRY: MW=2610; METHOD=FAST-AB.	
KW Antibiotic; Amphibian skin; Amidation.	
FT MOD-RES 25 25 AMIDATION.	
SQ SEQUENCE 25 AA; 2613 MW; OFF5A46EAQEAE12 CRC64;	
Query Match 9	
Best Local Similarity 19.2%; Score 24; DB 1; Length 25;	
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;	
QY 5 LPRLIARTSEH 15	
DB 14 IPHVVPVTAEH 24	
RESULT 9	
ID VIP_GADMO STANDARD; PRT; 25 AA.	
AC P09684; ID CO4_CAVPO STANDARD; PRT; 22 AA.	
DT 01-MAR-1989 (Rel. 10, Created)	
DT 01-MAR-1989 (Rel. 10, Last sequence update)	
DT 20-AUG-2001 (Rel. 40, Last annotation update)	
DE VASOACTIVE INTESTINAL PEPTIDE (VIP) (FRAGMENT).	
OS Gadus morhua (Atlantic cod).	
EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae;	
OC Gadus.	
NCBI_TAXID=8049;	
RN [1]	
RP SEQUENCE.	
RA Twwaites D.T., Young J., Thorndyke M.C., Dimaline R.;	
RT "Isolation and characterisation of two teleost VIP's.",	
RL Regul. Pept. 21:436-436(1988).	
CC -1- FUNCTION: VIP CAUSES VASODILATATION. LOWERS ARTERIAL BLOOD PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH AND GALL BLADDER.	
CC -1- MISCELLANEOUS: THERE IS ONLY A SINGLE DIFFERENCE BETWEEN THIS SEQUENCE AND THAT OF CHICKEN (ALA-19 INSTEAD OF VAL-19).	
CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.	
DR PIR; JQ061; JQ061.	
DR InterPro; IPR00032; Glucagon.	
DR Pfam; PF00123; hormone2_1.	
DR SMART; SM0070; GLUCA_1.	
DR PSICOGO; PS00260; GLUCAGON_1.	
KW Glucagon family; Hormone.	
FT NON-TER 25 25 ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE CAA ANAPHYLATOXIN.	
SQ SEQUENCE 25 AA; 2978 MW; 1573FF6F374DB7E4 CRC64;	
Query Match 9	
Best Local Similarity 35.7%; Pred. No. 1.2e+03;	
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;	
QY 11 FTSSHSHEFLKKGAA	
Db 6 FTDNYSRFRQMAA	
RESULT 10	
PVK2_PERAM STANDARD; PRT; 12 AA.	
ID PVK2_PERAM STANDARD; PRT; 12 AA.	
AC P81555; ID CO4_CAVPO STANDARD; PRT; 22 AA.	
DT 20-AUG-2001 (Rel. 40, Created)	
DT 20-AUG-2001 (Rel. 40, Last sequence update)	
DE PERIVISCROKININ-2 (PEA-PVK-2).	
OS Periplaneta americana (American cockroach).	
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;	
OC Blattidae; Blattidae; Periplaneta.	
NCBI_TAXID=6978;	
RN [1]	
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.	
RC TISSUE=Abdominal perisynaptic organs;	
RX MEDLINE=98326377; Pubmed=9653444;	
RA Prede R.; Repus J.; Ekerdt M.; Holman G.M.; Nachman R.J.; Wang Y.; Penzin H.;	
RA "Isolation of Periviscerokinin-2 from the abdominal perisynaptic organs of the American cockroach, <i>Periplaneta americana</i> ."; Peptides 19:801-805(1998).	
-1- FUNCTION: MYOACTIN; HAS EXCITATORY ACTIONS ON THE HYPERNEURAL MUSCLE.	
CC -1- MASS SPECTROMETRY: MW=1189.3; METHOD=MALDI.	
CC Neuropeptide; Amidation.	
FT MOD-RES 12 12 AMIDATION	
SQ SEQUENCE 12 AA; 1190 MW; 2F4D8EE1EB05728 CRC64;	
Query Match 9	
Best Local Similarity 18.4%; Score 23; DB 1; Length 12;	
Matches 3; Conservative 4; Mismatches 4; Indels 1; Gaps 0;	
QY 1 GMAPLPRL 8	
DB 5 GLISMPPRV 12	
RESULT 11	
CO4_CAVPO STANDARD; PRT; 22 AA.	
ID CO4_CAVPO STANDARD; PRT; 22 AA.	
AC P1969; ID CO4_CAVPO STANDARD; PRT; 22 AA.	
DT 01-NOV-1990 (Rel. 16, Created)	
DT 01-NOV-1990 (Rel. 16, Last sequence update)	
DT 01-FEB-1996 (Rel. 33, Last annotation update)	
DE COMPLEMENT C4 (FRAGMENT).	
GN C4.	
OS Cavia porcellus (Guinea pig).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Hstricognathi; Caviidae.	
NCBI_TAXID=10141;	
RN [1]	
RP SEQUENCE.	
RX MEDLINE=80227885; PubMed=7391069;	
RA Goldberger G.; Abraham G.N.; Williams J.; Colten R.R.;	
RT "NH2-terminal sequence analysis of pro-C4, the precursor of the fourth component of guinea pig complement.";	
RT J. Biol. Chem. 255:7071-7074(1980).	
CC -1- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE CAA ANAPHYLATOXIN.	
CC -1- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER	

* OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).

CC PIR; A17267; A17267.

DR InterPro; IPR001599; Alpha_2_macroglobulin.

DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; PARTIAL.

DR PROSITE; PS01178; ANAPHYLATOXIN_1; PARTIAL.

KW Complement pathway; Plasma; MHC III; Inflammatory response.

FT VARIANT 18 18 L->V.

FT NON-TER 22 22

SEQUENCE 22 AA; 2452 MW; 2CD16B54D0BB47A4 CRC64;

Query Match 18.4%; Score 23; DB 1; Length 22; Best Local Similarity 66.7%; Pred. No. 1.5e+03; Mismatches 4; Conservative 1; Indels 0; Gaps 0;

QY 6 PRLLAF 11 .

Db 2 PRLLLF 7

RESULT 12

CH60_THIEF

STANDARD; PRT; 23 AA.

AC P29134; |

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DR 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).

GN GROEL OR MOPA OR GROEL.

OS Thiobacillus ferrooxidans.

OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.

OX NCBI_TAXID=920; |

RN [1]

RP STRAIN=AVCC 19859;

RX MEDLINE=93093401; PubMed=1360930;

RA Varela P.; Jerez C.A.;

RT "Identification and characterization of GROEL and DnaK homologues in

RT Thiobacillus ferrooxidans";

RL FEMS Microbiol. Lett. 77:149-153(1992).

RN [2]

RP PHOSPHORYLATION.

RX MEDLINE=96242312; PubMed=9026439;

RA Seeger M.; Osorio G.; Jerez C.A.;

RT "Phosphorylation of GroEL, DnaK and other proteins from Thiobacillus ferrooxidans grown under different conditions";

RL FEMS Microbiol. Lett. 138:129-134(1996).

-I- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS

CONDITIONS (BY SIMILARITY).

-I- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STAKED RINGS OF

CC 7 SUBUNITS.

CC -I- INDUCTION: BY HEAT SHOCK.

CC -I- PTM: PHOSPHORYLATED ON THREONINE.

CC -I- MISCELLANEOUS: THIS PROTEIN SHOWS ATPASE ACTIVITY.

CC -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

DR HSSP; P06139; 1AON.

DR InterPro; IPR001840; Chaperonins_Cpn60.

DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.

FT Chaperone; ATP-binding; Heat shock; Phosphorylation.

FT NON_TER 23 23

SEQUENCE 23 AA; 2536 MW; 2BB6883872FB255D CRC64;

Query Match 18.0%; Score 22.5; DB 1; Length 23; Best Local Similarity 33.3%; Pred. No. 1.9e+03; Mismatches 5; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 9 IAPTFSEHSFLSLKG 23

Db 5 VAF-REHAREKMLRG 18

RESULT 13

LMT4_LOCMI

STANDARD; PRT; 13 AA.

AC P1450;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE LOCUSTAMYTROPIN 4 (LOM-MT-4).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Acridoidea; Acalyptrata; Orthopteroidea; Orthoptera; Caelifera;

OC Acrideromorpha; Acridoidea; Acridae; Locusta.

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain; Holman G.M., Hayes T.K., Nachman R.J.P., Kochansky J.P., Schoofs L., de Loof A.;

RT "Isolation, identification and synthesis of locustamytropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamytropin peptide family";

RT Insect Biochem. Mol. Biol. 22:447-452(1992).

RL CC -I- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY (MOTOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE STIMULATOR THAN LOM-MT I, II AND III.

CC -I- SIMILARITY: BELONGS TO THE PYRORININ FAMILY.

DR InterPro; IPR01484; Pyrarinin.

GN PROSITE; PS00539; PYRORININ; I.

KW Neuropeptide; Amidation; Pyrarinin.

FT MOD_RES 13 13 AMIDATION.

SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 17.6%; Score 22; DB 1; Length 13; Best Local Similarity 62.5%; Pred. No. 1.3e+03; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHAAALPRL 8

DB 6 GMFPSPRL 13

RESULT 14

CYCH_MOUSE

STANDARD; PRT; 18 AA.

AC Q61458;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE CYCLIN H (FRAGMENT).

GN CENH.

OS MUS musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NEBIL_TAXID=10090; |

RP SEQUENCE FROM N A.

RC STRAIN=GD-1; TISSUE=Testis;

RA Hall F.L., Wu L.; Submitted (Nov-1994) to the EMBL/GenBank/DBJ databases.

CC -I- FUNCTION: MEMBER OF CAK WHICH ACTIVATES CYCLIN ASSOCIATED

CC CDK2/CDK3/CDK4 BY THREONINE PHOSPHORYLATION. ITS EXPRESSION AND

CC ACTIVITY ARE CONSTANT THROUGHOUT THE CELL CYCLE. CAK IS TIGHTLY ASSOCIATED WITH A MULTIPROTEIN COMPLEX THAT, WHICH PLAYS A DUAL

CC ROLE IN TRANSCRIPTION AND DNA REPAIR (BY SIMILARITY).

CC -I- SUBUNIT: MAMMALIAN CAK CONTAINS THREE COMPONENTS: CDK7, CYCLIN H,

CC -I- AND AN ASSEMBLY FACTOR CALLED MAT1.

CC -I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC DR EMBL: X82441; CAA57822; 1; -
 DR HSP; P51946; 1KXU.
 DR Interpro; IPR000553; Cyclin.
 DR PROSITE; PS00292; CYCLINS; PARTIAL.
 KW Cyclin; Cell cycle; Cell division; Nuclear protein;
 KW transcription regulation.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2105 MW; 92964DCF68EB98C7 CRC64;

Query Match 17.6%; Score 22; DB 1; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.8e+03; 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PRLIATF 12
 Db 10 PRIMLT 16

RESULT 15
 FAR7_ASCSU STANDARD; PRT; 8 AA.
 ID FAR7_ASCSU SPECIES=F.coli; STRAIN=K12 / MG1655;
 AC P4_711; MEDLINE=97122661; PubMed=360215;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-AUG-1996 (Rel. 33, Last annotation update)
 DT FMRFAMIDE-LIKE NEUROPEPTIDE AF7.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nemata; Chromadorea; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TAXID=6233;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=35380362; PubMed=7651904.
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
 RT Ascaris suum";
 RL Peptides 16:411-500(1995).
 CC -I SIMILARITY: BELONGS TO THE FMRP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 963 MW; 9CD40059DA17687D CRC64;

Query Match 16.8%; Score 21; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+05; 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PRLIJAF 11
 Db 3 PREFIRF 8

RESULT 16
 LPHI_ECOLI STANDARD; PRT; 16 AA.
 ID LPHI_ECOLI SPECIES=E.coli; STRAIN=K12, AND LT2;
 AC P03058; MEDLINE=89094829; PubMed=306217;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HIS OPERON LEADER PEPTIDE (ATTENUATOR PEPTIDE).
 GN HISL OR B2018.
 OS Escherichia coli, and Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia,
 OX NCBI_TAXID=562; 602;
 RN [1]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; and S.typhimurium; STRAIN=K12, AND LT2;
 RX MEDLINE=89094829; PubMed=306217;
 RA Carlonagno M.S., Chiarootti L., Alifano P., Nappo A.G., Bruni C.B.;
 RT "Structure and function of the *Salmonella typhimurium* and *Escherichia
 coli* K-12 histidine operons.";
 RL J. Mol. Biol. 203:585-606(1988).
 RN [2]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=82039525; PubMed=6170941;
 RA Verde P., Frunzio R., di Nocera P.P., Blasi F., Bruni C.B.;
 RT "Identification, nucleotide sequence and expression of the regulatory
 region of the histidine operon of *Escherichia coli* K-12.";
 RL Nucleic Acids Res. 9:2075-2086(1981).
 RN [3]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=79033821; PubMed=6170941;
 RA Dincera P.P., Blasi F., Dilauro R., Frunzio R., Bruni C.B.;
 RT "Nucleotide sequence of the attenuator region of the histidine operon
 of *Escherichia coli* K-12.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:4276-4280(1978).
 RN [4]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97122661; PubMed=3278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rose C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [5]
 SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2;
 RX MEDLINE=79033822; PubMed=360216;
 RA Barnes W.M.;
 RT DNA sequence from the histidine operon control region: seven
 histidine codons in a row";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:4281-4285(1978).
 RN [6]
 SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2;
 RA Barnes W.M., Russon R.N., Whittier R.;
 RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE ATTENUATION MECHANISM
 CC FOR THE CONTROL OF THE EXPRESSION OF THE HIS STRUCTURAL GENES.

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CC EMBL; V00385; CAA23550.1; -
 DR EMBL; V00384; CAA23548.1; -
 DR EMBL; X13662; CAA31310.1; -
 DR EMBL; V01371; CAA24556.1; -
 DR EMBL; AE000293; AAC15079.1; -
 DR EMBL; X13664; CAA31311.1; -
 DR EMBL; J01804; AAA88313.1; -
 DR PIR; A03594; LFECCH
 DR Ecogene; EG11269; hsl.
 DR StyGene; SG10166; hsl.
 KW Histidine biosynthesis; Leader peptide; Complete proteome.
 SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 16.8%; Score 21; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 2.3e+03; Mismatches 5; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 TAFTSHSH 17
 Db 4 VQFKHHHH 12

RESULT 17
 SETB_SALTY STANDARD PRT; 22 AA.
 ID SETB_SALTY PRT; 22 AA.
 AC P33027;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SUGAR_EFLUX TRANSPORTER B (FRAGMENT)
 GN SETB.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TAXID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89313634; PubMed=2546043;
 RA Geisse R.H., Izzo P.W.; Postma P.W.;
 RT "The PEP: fructose Phosphotransferase system in *Salmonella* L-Mol. Gen. Genet. 216:517-525(1989).
 RL Typhimurium: FPR combines enzyme IIIFru and pseudo-HPr activities.";
 CC -1- FUNCTION: INVOLVED IN THE EFFLUX OF SUGARS. THE PHYSIOLOGICAL ROLE
 MAY BE THE DETOXIFICATION OF NON-METABOLIZABLE SUGAR ANALOGS. CAN
 TRANSPORT LACTOSE AND GLUCOSE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 (PROBABLE);
 CC -1- SIMILARITY: BELONGS TO THE SET FAMILY OF TRANSPORTERS.
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 CC
 DR EMBL; X11423; -; NOT_ANNOTATED_CDS.
 DR StyGene; SG10423; setB.
 DR Transport; Sugar transport; Transmembrane; Inner membrane.
 FT TRANSMEM 13 >22 POTENTIAL.
 FT NON_TER 22 22
 SEQUENCE 22 AA; 2291 MW; 2849C330172CC5C2 CRC64;

Query Match 16.8%; Score 21; DB 1; Length 24;
 Best Local Similarity 33.3%; Pred. No. 3.5e+03; Mismatches 1; Indels 2; Gaps 1;
 Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 GMAA-LPRL 9
 Db 7 GLAAANFLPITI 17

RESULT 19
 ALLI-CYDPO STANDARD PRT; 8 AA.
 ID ALLI-CYDPO
 AC P82152;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYDASTATIN 1.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidea; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TAXID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=larva;
 RX MEDLINE=9805459; PubMed=932829;
 RA Dube H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East D.D., Thorpe A.;
 RT "Lepidopteran Peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 MOD_RES 8 AMIDATION.
 SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 16.8%; Score 21; DB 1; Length 22;
 Best Local Similarity 45.5%; Pred. No. 3.2e+03; Mismatches 5; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 ALAPRILAFFS 13
 Db 7 AAAPRSFDTS 17

RESULT 18
 GAE6_RANRU STANDARD PRT; 24 AA.
 ID GAE6_RANRU
 AC P80400;
 DT 01-NOV-1995 (Rel. 32, Created).
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GREGORIN 6.
 OS Rana rugosa (Frog); Eukaryota; Chordata; Craniata; vertebrates; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

Query Match 16.0%; Score 20; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+05; Mismatches 3; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 13 SEHSHSL 20
 Db .1 SPHYNFGI 8

RESULT 20
 GLEM_HUMAN STANDARD PRT; 10 AA.
 ID GLEM_HUMAN
 AC P02728;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ERTHROCYTE MEMBRANE GLYCOPAPTIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=2034940; PubMed=5386550;
RA Weiss J.B., Lotte C.J., Bobinski H.;
RT "New low molecular weight glycopptide containing triglycosylcysteine
in human erythrocyte membrane."
RL Nature New Biol. 234:25-26(1971).
CC -1 PTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-Glc TRISACCHARIDE.
CC -1 MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS
PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED.
CC PIR: A03187; XGRHOB.
KW Glycoproteins; Erythrocyte.
FT CABOHYD 1 S-LINKED (GLC:1'.').
SQ SEQUENCE 10 AA; 1049 MW; 239BFEEAA1F5B1E8 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mishatches 0; Indels 0; Gaps 0;

Qy 15 HSH 17
Db 4 HSH 6

RESULT 21
GONI_PETMA STANDARD; PRT; 10 AA.
ID GONI_PETMA
AC P04378;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE GONADOLIBERIN I (GONADOTROPIN RELEASING HORMONE I) (GNRH-I)
DE (LUTLIBERIN I)
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
QX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RC TISSUE_Brain;
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT Primary structure of gonadotropin-releasing hormone from lamprey
brain.';
RL J. Biol. Chem. 261:4812-4819(1986).
CC -1 FUNCTION: STIMULATES THE RELEASE OF BOTH LUTEINIZING AND
FOLLICLE-STIMULATING HORMONES.
CC -1 SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR PIR: A01412; RHMGS.
DR InterPro: IPR002012; GnrH.
DR Pfam: PF00446; GnrH; 1.
DR PROSITE: PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus.
FT MOD-RES 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD-RES 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; 1E4B162371735AB CRC64;

Query Match 16.0%; Score 20; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mishatches 0; Indels 0; Gaps 0;

Qy 17 HFSLK 21
Db 2 HYSLE 6

RESULT 22
ASPL_LACSN STANDARD; PRT; 15 AA.
ID ASPL_LACSN
AC P82648;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ACID SHOCK PROTEIN 1 (FRAGMENTS).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Bacillales/Clostridiales; Lactobacillaceae;
OC Lactobacillus.
QX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CB1;
RX Published=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbiotti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -1 INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 SLKKG 23
Db 1 SFRKKG 5

RESULT 23
MCA2_RHOOP STANDARD; PRT; 15 AA.
ID MCA2_RHOOP
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE PUTATIVE MALEYLACETATE REDUCTASE II (EC 1.3.1.32) (FRAGMENT).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriidae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcaceae.
QX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=ICP;
RX MEDLINE=98324954; Published=98324954;
RA Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
Rhodococcus opacus ICP.";
RL J. Bacteriol. 180:3503-3508(1998).
CC -1 CATALYTIC ACTIVITY: 3-OXOALIDATE + NAD(P)(+) = 2-MALEYLACETATE +
NAD(P)H.
CC PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -1 SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL-DEHYDROGENASE
FAMILY.
DR InterPro: IPRE001670; Fe-ADH.
DR PROSITE: PS00913; ADH-IRON_1; PARTIAL.
DR PROSITE: PS00060; ADH-IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NOR_TER 15 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD0388025E CRC64;

Query Match 16.0%; Score 20; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPRLTAF 11
ID DFTS_RAT STANDARD; PRT; 20 AA.
AC ||: |
ID DFTS_RAT STANDARD; PRT; 20 AA.
AC ||: |
DT 01-APR-1998 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE DENTINAL FLUID TRANSPORT-STIMULATING PEPTIDE (DFT-STIMULATING PEPTIDE)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Parotid gland;
RX MEDLINE=87131231; PubMed=3815601;
RA Yamamoto T., Kobayashi M., Kobayashi M., Yamamoto M., Nomura M.,
RA Nonuma S.;
RT "Isolation and amino acid sequence of dentinal fluid transport-
stimulating peptide from rat Parotid glands.";
RL Chem. Pharm. Bull. 34:3803-3811(1986).
RN [2]
CHARACTERIZATION.
RX MEDLINE=67131708; PubMed=5297832;
RA Steinman R.R.;
RT "The movement of acriflavine hydrochloride through molars of rats on
a cariogenic and non-cariogenic diet.";
RL J. South. Calif. Dent. Assoc. 35:151-157(1967).
CC WHICH IS IMPORTANT FOR THE PREVENTION OF DENTAL CARIES.
DR PIR; JJ0001; DIR;
KW Dental caries; Parotid gland; Hormone;
SEQUENCE 20 AA; 2165 MW; FA164F2B0AF80D5A CRC64;

Query Match 16.0%; Score 20; DB 1; Length 20;
Best Local Similarity 27.8%; Pred. No. 4.2e+03;
Matches 5; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 8 LIRITSEHHSFSKKGAA 25
Db 2 VIAMELQHNEPGRKDSTA 19

RESULT 25
LPTB_BACST STANDARD; PRT; 20 AA.
ID LPTB_BACST STANDARD; PRT; 20 AA.
AC P05258;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TETRACYCLINE RESISTANCE LEADER PEPTIDE.
GN TETL.
OS Bacillus stearothermophilus, *Bacillus cereus*, and
OS *Staphylococcus hyicus*.
OG Plasmid pTH15, Plasmid pBC16, and Plasmid pTETL.
OC Bacteria; Firmicutes; *Bacillus/Clostridium* group;
Bacillus/Staphylococcus group; Geobacillus.
OX NCBI_TaxID=1422, 1396, 1284;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=pTH15;
MEDLINE=86031344; PubMed=2996983;
RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
"Nucleotide sequence of the tetracycline resistance gene of pTH15, a

RT thermophilic *Bacillus* plasmid: comparison with staphylococcal *tcr* controls.; Gene 37:131-138(1985).
RL Gene 37:131-138(1985).
RN [2]
SEQUENCE FROM N.A.
RP PLASMID=pBC15;
RC RX MEDLINE=90221899; PubMed=2109312;
RA Palva A., Virolainen G., Simonen M., Rintala H., Laamanen P.;
RT "Nucleotide sequence of the tetracycline resistance gene of pBC15 from *Bacillus cereus*." Nucleic Acids Res. 18:1635-1635(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S. hyicus; PLASMID=pTETL;
RX MEDLINE=92321725; PubMed=1622166;
RA Schwarz S., Cardoso M., Wedener H.C.;
RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline resistance determinant encoded by plasmid pTETL from *Staphylococcus hyicus*". Antimicrob. Agents Chemother. 36:580-588(1992).
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CC DR EMBL; D00006; BA00004.1; -.
DR EMBL; M11036; AA022850.1; -.
DR EMBL; X51366; CA035750.1; -.
DR PIR; S09233; LFSTNU.
DR PIR; S23742; S23742.
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 20 AA; 2253 MW; 18D0F4A6CA031CA1 CRC64;

Query Match 16.0%; Score 20; DB 1; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.2e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 13 SEHSHFSKKGAA 24
Db 4 NBCNRVOLKEGS 15

Search completed: January 6, 2002, 09:57:10
Job time: 276 sec

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Gencore version 4.5

OM protein - protein search, using sw mode

Run on:	January 6, 2002, 09:51:49	Search time 22.2 Seconds (without alignments)
Title:	US-09-441-061-2	164.721 Million cell updates/sec
Perfect score:	125	
Sequence:	GMAALPRLAFTSBSHFSLKKGAA	25
Scoring table:	BLOSUM62	
	Gapop 10.0	, Gapext 0.5
Searched:	473505 seqs,	146272329 residues
Total number of hits satisfying chosen parameters:	7775	
Minimum DB seq length:	0	
Maximum DB seq length:	25	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
Database :	Listing first 50 summaries	
	SPTREMBL_17:*	
	1:	sp_archea:*
	2:	sp_bacteria:*
	3:	sp_fungi:*
	4:	sp_human:*
	5:	sp_invertebrate:*
	6:	sp_mammal:*
	7:	sp_mhc:*
	8:	sp_organelle:*
	9:	sp_phage:*
	10:	sp_plant:*
	11:	sp_rabbit:*
	12:	sp_virus:*
	13:	sp_vertebrate:*
	14:	sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match Length	DB ID	Description
1	32	25.6	2 O26056	O26056 helicobacte
2	30	24.0	20 P79837	P79837 prioniumluru
3	27	21.6	25 040354	Q40354 mediavirga sa
4	26.5	21.2	24 Q9TN55	Q9TN55 homo sapien
5	26	20.8	9 Q9VVB2	Q9VVB2 drosophila
6	26	20.8	15 Q9TRP0	Q9TRP0 sus scrofa
7	26	20.8	23 Q9R314	Q9R314 helicobacte
8	26	20.8	24 016333	Q16333 homo sapien
9	25	20.0	15 092093	Q92093 rattus norv
10	25	20.0	23 Q9NB03	Q9NB03 chironomus
11	25	20.0	23 097081	Q97081 pseudorabde
12	25	20.0	24 Q16061	Q16061 homo sapien
13	25	20.0	24 092833	Q92833 rana berlian
14	25	20.0	24 P82334	P82334 rana berlian
15	25	20.0	24 P82338	P82338 rana berlian
16	25	20.0	25 Q9BTR5	Q9BTR5 homo sapien
17	25	20.0	25 060339	Q90839 mus musculu
18	25	20.0	25 063999	Q93999 rattus norv
19	25	20.0	25 064000	Q94000 rattus norv

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution

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20	21	22	22	24	24	25
21	22	23	23	24	24	25
22	23	24	24	25	25	26
23	24	25	25	26	26	27
24	25	26	26	27	27	28
25	26	27	27	28	28	29
26	27	28	28	29	29	30
27	28	29	29	30	30	31
28	29	30	30	31	31	32
29	30	31	31	32	32	33
30	31	32	32	33	33	34
31	32	33	33	34	34	35
32	33	34	34	35	35	36
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34	35	36	36	37	37	38
35	36	37	37	38	38	39
36	37	38	38	39	39	40
37	38	39	39	40	40	41
38	39	40	40	41	41	42
39	40	41	41	42	42	43
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41	42	43	43	44	44	45
42	43	44	44	45	45	46
43	44	45	45	46	46	47
44	45	46	46	47	47	48
45	46	47	47	48	48	49
46	47	48	48	49	49	50
47	48	49	49	50	50	51
48	49	50	50	51	51	52
49	50	51	51	52	52	53
50	51	52	52	53	53	54

ALIGNMENT

09yp14	lucerne tra
09uc55	homo sapien
09byf2	homo sapien
09tw57	lamellibrac
09ps15	oncorhynchus
09wg33	bacillus ha
09wf67	gallus gall
09zs60	lycopersicu
09bm59	sagitta sp.
09cv03	mus musculu
09uj91	homo sapien
09ws69	leucophaea
09ms42	canis famili
09znt6	onyx brach
09bs65	bos tauru
094s39	klipsela
09un59	homo sapien
09nn23	homo sapien
001246	human para
034219	pedomorpha
09zg42	chlamydia t
026833	trypanosoma
014559	homo sapien
09qy63	rattus sp.
09sy23	arabidopsis
09q121	muss musculi
09la84	rhabdother
09in10	mus musculu
032825	rana luteo
09rg92	lactobacill

20	21	22	22	24	24	25
21	22	23	23	24	24	25
22	23	24	24	25	25	26
23	24	25	25	26	26	27
24	25	26	26	27	27	28
25	26	27	27	28	28	29
26	27	28	28	29	29	30
27	28	29	29	30	30	31
28	29	30	30	31	31	32
29	30	31	31	32	32	33
30	31	32	32	33	33	34
31	32	33	33	34	34	35
32	33	34	34	35	35	36
33	34	35	35	36	36	37
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36	37	38	38	39	39	40
37	38	39	39	40	40	41
38	39	40	40	41	41	42
39	40	41	41	42	42	43
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41	42	43	43	44	44	45
42	43	44	44	45	45	46
43	44	45	45	46	46	47
44	45	46	46	47	47	48
45	46	47	47	48	48	49
46	47	48	48	49	49	50
47	48	49	49	50	50	51
48	49	50	50	51	51	52
49	50	51	51	52	52	53
50	51	52	52	53	53	54

Matches	8;	Conservative	1;	Mismatches	7;	Indels	0;	Gaps	0;	QY	4 ALPRLIQAF 11
QY	8 LIAFTSEHSHPSLKG 23									D9	1
Db	2 LIAFYFRFLDSLKRG 17									D9	2 AAPRQIAF 9
RESULT 2											
ID	P79837; PRELIMINARY;	PRT;	20 AA.							Q9TNS5; PRELIMINARY;	PRT;
AC	P79837; PRELIMINARY; 03; Created)									AC Q9TNS5; PRELIMINARY;	PRT; 24 AA.
DT	01-MAY-1997 (TREMBLrel. 03; Last sequence update)									DT 01-MAY-2000 (TREMBLrel. 13; Created)	
DT	01-MAY-1997 (TREMBLrel. 03; Last annotation update)									DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)	
DT	01-MAY-1997 (TREMBLrel. 03; Last annotation update)									DT 01-JUN-2000 (TREMBLrel. 14; Last annotation update)	
DE	INDURONATE 2-SULFATASE (FRAGMENT).									OS HUMAN LEUCOCYTE ANTIGEN BETA CHAIN DR MOLECULE HLA-DRB1 (FRAGMENT).	
OS	Prionailurus bengalensis (leopard cat).									OS Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.									OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=37029;									OX NCBI_TaxID=9606;	
RN	[1]									RN [1]	
RP	SEQUENCE FROM N.A.									RP SEQUENCE FROM N.A.	
RA	Dyons L.A.; Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E., O'brien S.J.									RA RX MEDLINE=93107319; PubMed=1469092;	
RA	RA "The HLA-DRB1 locus as a genetic component in giant cell arteritis.									RA Weyand C.M., Hickok K.C., Hunter G.C., Goronzy J.J.; RT Mapping of a disease-linked sequence motif to the antigen binding site of the HLA-DR molecule."	
RL	Nat. Genet. 15:0-0(0); DR EMBL; US1266; AAB39359; 1; -.									RL J. Clin. Invest. 90:2355-2361(1992).	
FT	NON_TER 1									KW MHC.	
FT	NON_TER 20									SQ SEQUENCE 24 AA; 3019 MW; 4A23BF7821BACCE0 CRC64;	
SQ	SEQUENCE 20 AA; 2081 MW; 7D009D35F57AE228 CRC64;										
Query Match Score 24.08; Best Local Similarity 62.58%; Matches 5; Conservative 5; Mismatches 2; Indels 1; Gaps 0;											
Query Match Score 24.08; Best Local Similarity 62.58%; Prod. No. 4.5e+02; Matches 5; Conservative 5; Mismatches 2; Indels 1; Gaps 0;											
QY	8 LIAFTSEH 15									QY 12 TSEHSHS----LKKG 23	
Db	13 IIAFASDH 20									Db 5 TSEHDYFHNNDAYLQKG 21	
RESULT 3											
ID	Q40354; PRELIMINARY;	PRT;	25 AA.							Q9VVB2; PRELIMINARY;	PRT; 9 AA.
AC	Q40354; PRELIMINARY; 01; Created)									AC Q9VVB2; PRELIMINARY;	PRT; 9 AA.
DT	01-NOV-1996 (TREMBLrel. 01; Last sequence update)									DT 01-MAY-2000 (TREMBLrel. 13; Created)	
DT	01-JUN-2001 (TREMBLrel. 17; Last annotation update)									DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)	
DE	MOS GENE (REQUIRED FOR SYNTHESIS OF L-3-O-METHYL-SCYLLO-INOSAMINE (3-O-MSI)), 5' END AND PROMOTER REGION (FRAGMENT).									DE CG18219 PROTEIN (FRAGMENT).	
GN	MOS									GN CG18219.	
OS	Drosophila melanogaster (Fruit fly).									OS Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha.									OC Ephydriidae; Drosophilidae; Drosophila.	
OC	RC STRAIN-BERKELEY FROM N.A.									RC RN NCBI_TaxID=72277;	
RN	SEQUENCE FROM N.A.									RN [1]	
RP	SEQUENCE FROM N.A.									RP SEQUENCE FROM N.A.	
RX	MEDLINE=89057889; PubMed=2848255;									RX RC STRAIN-BERKELEY FROM N.A.	
RA	Murphy P.J., Heycke N., Trezz S.P., Raret P., De Brujin F.J., Scheff J.; Synthesis of an opine-like compound, a rizopine, in alfalfa nodules symbiotically regulated.";									RA RX MEDLINE=20196006; PubMed=10731132;	
RA	Proc. Natl. Acad. Sci. U.S.A. 85:9133-9137 (1988). InterPro: IPR000392; NitrogenaseII.									RA RA Adams M.D., Celikin R.S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Charape M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayali A., An H.-J., Baldwin R.M., Basu A., Baxendale J., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchkine P., Bouck M.R., Borukov S., Burrows K.C., Busam D.A., Butler H., Cadieu E., Chandrasekaran P., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodzik A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Globok A.,	
RA	DR PFM: PF00142; fer4_NIFH; 1.									RA RA Adams M.D., Celikin R.S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Charape M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayali A., An H.-J., Baldwin R.M., Basu A., Baxendale J., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchkine P., Bouck M.R., Borukov S., Burrows K.C., Busam D.A., Butler H., Cadieu E., Chandrasekaran P., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodzik A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Globok A.,	
FT	25 AA; 2685 MW; 1F22739287210F82 CRC64;									RA RA Adams M.D., Celikin R.S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Charape M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayali A., An H.-J., Baldwin R.M., Basu A., Baxendale J., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchkine P., Bouck M.R., Borukov S., Burrows K.C., Busam D.A., Butler H., Cadieu E., Chandrasekaran P., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodzik A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Globok A.,	
SQ	Query Match Score 21.6%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Mismatches 0; Indels 2; Gaps 0;									RA RA Adams M.D., Celikin R.S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Charape M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayali A., An H.-J., Baldwin R.M., Basu A., Baxendale J., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchkine P., Bouck M.R., Borukov S., Burrows K.C., Busam D.A., Butler H., Cadieu E., Chandrasekaran P., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodzik A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Globok A.,	

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai J., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishina N.V., Mobarry C., Morris J., Mosiref A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purli V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of *Drosophila melanogaster*."; RL *Science* 287:2165-2195(2000).; DR EMBL: AE00526; AACF4371; -; FRT NON-TER 1 1 SEQUENCE 9 AA; 975 MW; F31AB472045B9C1 CRC64;

Query Match 20.8%; Score 26; DB 5; Length 9; Best Local Similarity 55.6%; Pred. No. 4.7e+05; Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0; ID QY 16 SHFSIKRGA 24 PRELIMINARY; PRT; 15 AA.

Db 1 SHFSILNSA 9

RESULT 6

Q9TRPO PRELIMINARY; PRT; 15 AA.

ID Q9TRPO; AC 01-MAY-2000 (TREMBREL, 13, Created) DT 01-MAY-2000 (TREMBREL, 13, Last sequence update) DT 01-JUN-2000 (TREMBREL, 14, Last annotation update) DE LOW MR ZONA PELLUCIDA BINDING PROTEIN (FRAGMENT). OS Sus scrofa (Pig) SEQUENCE FROM N.A. RN [1] RP MEDLINE=93378826; PubMed=1510840; RX RA Parry R.V., Barker P.J., Jones R.; RT "Characterization of low Mr zona pellucida binding proteins from boar spermatozoa and seminal plasma."; RL Mol. Reprod. Dev. 33:108-115(1992); RT SEQUENCE 15 AA; 1525 MW; CC800E1028CF2058 CRC64;

Query Match 20.8%; Score 26; DB 6; Length 15; Best Local Similarity 44.4%; Pred. No. 1.5e+03; Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0; ID QY 3 AAIPRLIAF 11 PRELIMINARY; PRT; 23 AA.

Db 7 AAIPQSWVFE 15

RESULT 7

Q93A14 ID Q93A14 PRELIMINARY; PRT; 23 AA.

AC 01-MAY-2000 (TREMBREL, 13, Created) DT 01-MAY-2000 (TREMBREL, 13, Last sequence update) DT 01-MAY-2000 (TREMBREL, 13, Last sequence update)

Query Match 20.8%; Score 26; DB 4; Length 24; Best Local Similarity 44.4%; Pred. No. 2.5e+03; Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0; ID QY 10 AFNSESHHF 18 PRELIMINARY; PRT; 15 AA.

Db 7 AFNSESHHF 18

RESULT 9

Q9ZD03 ID Q9ZD03 PRELIMINARY; PRT; 15 AA.

AC 01-MAY-1999 (TREMBREL, 10, Created) DT 01-MAY-1999 (TREMBREL, 10, Last sequence update) DT 01-MAY-1999 (TREMBREL, 10, Last annotation update) DE SNO ONCOPROTEIN (FRAGMENT).

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Vedyo C.G., Sogayar M.C.;
 RT Cloning of glucocorticoid-regulated sequences using equalizing CDNA
 subtraction based on selective suppression of polymerase chain
 reaction in rat C6/ST1 glioma phenotypic reversion.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 DR AF112446; AAD17200.1;
 FT NON_TER 15 15 AA; 1667 MW; D2F5236DE2647B80 CRC64;

SEQUENCE 15 AA; 1667 MW; D2F5236DE2647B80 CRC64;
 Query Match Score 20.0%; Best Local Similarity 55.6%; Length 15;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 16 SHFSIKRGA 24
 Db 6 SNFSLVQGS 14

RESULT 10
 ID Q9NBD9 PRELIMINARY; PRT; 23 AA.

AC Q9NBD9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HEMOGLOBIN 11B (FRAGMENT).
 GN GB2B.
 OS Chironomus neapeanensis.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Tracheata; Hexapoda; Nematocera;
 OC Chironomoidea; Chironomidae; Chironominae; Chironomus.
 OC NCBI_TAXID=13501;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Grimaldi M.C., Scherbk S.V., Almanova K.G., Blinov A., Diez J.-L.,
 RA Bergstrom G.; Scherbk S.V., Almanova K.G., Blinov A., Diez J.-L.,
 RT "Insect globin gene polymorphisms: Intronic minisatellites and a
 RT retroposon interrupting exon 1 of homologous globin genes in
 RT Chironomus (Diptera)." Gene 251:153-163 (2000);
 RL Gene 251:153-163 (2000);
 DR EMBL; AF250305; AAF87714.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 23 AA; 233 MW; 3B0BF7A8FAB5EF33 CRC64;

Query Match Score 20.0%; Best Local Similarity 50.0%; Length 23;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 7 RLLIAFTSE 14
 Db 6 RIVGFVSE 13

RESULT 11
 ID Q87081 PRELIMINARY; PRT; 23 AA.

AC Q87081;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE GLYCOPROTEIN C PRECURSOR (FRAGMENT).
 GN GC
 OS Pseudorabies virus.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TAXID=10345;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BECKER;
 RX MEDLINE=96070924; PubMed=7499261;
 RA Ryan P., Edwards C.O.;
 RT "Systematic introduction of proline in a eukaryotic signal sequence
 suggests asymmetry within the hydrophobic core." J. Biol. Chem. 270:27876-27879 (1995).
 RL EMBL; U29124; AAC54534.1; -.
 DR AAC54534.1;
 FT SIGNAL.
 SQ FT SIGNAL 1 22 POTENTIAL.
 FT NON_TER 23 23 MW; B7112B05ED406F3F CRC64;

SEQUENCE 23 AA; 2229 MW; B7112B05ED406F3F CRC64;
 Query Match Score 20.0%; Best Local Similarity 66.7%; Length 23;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 MAALPRLIA 10
 Db 8 MILALPALYA 16

RESULT 12
 ID Q16061 PRELIMINARY; PRT; 24 AA.

AC Q16061;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE TNNT1 PROTEIN (FRAGMENT).
 GN TNNT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=9006597; PubMed=8403232;
 RA Novelli G., Gemarelli M., Sangiulio F., D'Agruma L., Lo Cicero S.,
 RA Melchionda S., DallaPiccola B.;
 RT "Isolation and cloning of a polymerase chain reaction of a genomic DNA
 fragment of the human slow skeletal tropomodulin (TNNT1) gene." Cell Biochemistry and Function 11:187-191 (1993).
 RL DR EMBL; S66057; AAD13978.1;
 DR EMBL; S66170; AAD13978.1; JOINED.
 DR EMBL; S66170; AAD13978.1; JOINED.
 FT NON_TER 24 24 MW; 4A41B1A59FD34E5E CRC64;

SEQUENCE 24 AA; 274 MW; 4A41B1A59FD34E5E CRC64;
 Query Match Score 20.0%; Best Local Similarity 55.6%; Length 24;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 16 SHFSIKRGA 24
 Db 6 SHAQKRKGA 14

RESULT 13
 ID P82833 PRELIMINARY; PRT; 24 AA.
 AC P82833;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE BREVININ1BA.
 OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OC NCBI_TaxID=30360;
 RN [1]
 RP PRELIMINARY; FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN;
 RX MEDLINE-2011700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E., Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families isolated from the skins of the North American frogs Rana luteiventris, Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -I- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 CC S. AUREUS.
 CC -I- MASS SPECTROMETRY: MW=263; METHOD=ELECTROSPRAY.
 CC -I- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.
 KW Antibiotic.
 FT DISULFID 18 24 BY SIMILARITY.
 SQ SEQUENCE 24 AA; 2645 MW; CB524A45447DF4 CRC64;

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03; Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
 CC DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 Db 7 GMAAKFLPKIFCAISK 22

RESULT 14
 P82834 PRELIMINARY; PRT; 24 AA.
 AC P82834;
 ID P82834;
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE BREVININ-1BB.
 OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 NCBI_TaxID=30360;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN;
 RX MEDLINE-2011700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E., Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families isolated from the skins of the North American frogs Rana luteiventris, Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -I- MASS SPECTROMETRY: MW=263; METHOD=ELECTROSPRAY.
 CC -I- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.
 KW Antibiotic.
 FT DISULFID 18 24 BY SIMILARITY.
 SQ SEQUENCE 24 AA; 2631 MW; CB524A454434CF4 CRC64;

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03; Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
 CC DE 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 Db 7 GMAAKFLPKIFCAISK 22

RESULT 16
 Q9BTR5 PRELIMINARY; PRT; 25 AA.
 ID Q9BTR5
 AC Q9BTR5;
 DT 01-JUN-2001 (TREMBLrel. 17, created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DE UNKNOWN (PROTEIN FOR IMAGE:3451158) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.
 NCBI_TaxID=9605;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CHORIOCARCINOMA;
 RA Straubberg R.;
 CC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC003414; AAH03414.1;
 DR EMBL; BC003414; AAH03414.1;
 FT NON_TER 1 1
 SQ SEQUENCE 25 AA; 2625 MW; BB649418A85ABD5 CRC64;

Query Match 20.0%; Score 25; DB 13; Length 24;
 Best Local Similarity 43.8%; Pred. No. 3.6e+03; Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
 CC DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 Db 7 GMAAKFLPKIFCAISK 22

RESULT 17

Q60839; ID Q60839; AC Q60839; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update); DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update); DE ALPHA-1-ACID GLYcoprotein 2 (FRAGMENT). OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus. NCBI_TAXID=10116; [1]	PRELIMINARY; PRT; 25 AA. SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=LIVER; RA Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases. DR U24278; AAA91124.1; FT NON_TER 25 ; SEQUENCE 25 AA; 2843 MW; 8C7FED577021D463 CRC64; Qy 8 LIAFTSEHSHFSL 20 Db 2 LEAQNPHEANFTI 14	Score 20.0%; Best Local Similarity 38.5%; Pred. No. 3.8e+0; Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;	RESULT 18 Q63999; ID Q63999; AC Q63999; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update); DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update); DE VASOPRESSIN (FRAGMENT). OS Rattus norvegicus (Rat). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus. NCBI_TAXID=10116; [1]	SEQUENCE FROM N.A. MEDLINE=94286516; PubMed=8016115; RA Van Leeuwen F.W.; RT "Frameshift mutations at two hotspots in vasopressin transcripts in post-mitotic neurons."; RL Proc. Natl. Acad. Sci. U.S.A. 91:6059-6063(1994). DR S71427; AAB31127.1; -; FT NON_TER 1 ; SEQUENCE 25 AA; 2455 MW; B1FIESEAD310F237 CRC64; Qy 3 AALPRLIA 10 Db 4 AALPRASA 11	Score 25; DB 11; Length 25; Best Local Similarity 20.0%; Pred. No. 3.8e+0; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Q64000; ID Q64000; AC Q64000; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update); DE VASOPRESSIN (FRAGMENT). OS Rattus norvegicus (Rat).	PRELIMINARY; PRT; 25 AA. SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=LIVER; RA Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases. DR U24278; AAA91124.1; FT NON_TER 25 ; SEQUENCE 25 AA; 2458 MW; 4D78687ACF623E59 CRC64; Qy 3 AALPRLIA 10 Db 4 AALPRASA 11	Score 25; DB 11; Length 25; Best Local Similarity 75.0%; Pred. No. 3.8e+0; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	RESULT 19 Q64000; ID Q64000; AC Q64000; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update); DE VASOPRESSIN (FRAGMENT). OS Rattus norvegicus (Rat).	PRELIMINARY; PRT; 25 AA. SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=LIVER; RA Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases. DR U24278; AAA91124.1; FT NON_TER 25 ; SEQUENCE 25 AA; 2458 MW; 4D78687ACF623E59 CRC64; Qy 3 AALPRLIA 10 Db 4 AALPRASA 11	Score 25; DB 12; Length 25; Best Local Similarity 20.0%; Pred. No. 3.8e+0; Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Q64000; ID Q64000; AC Q64000; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update); DE VASOPRESSIN (FRAGMENT). OS Rattus norvegicus (Rat).	PRELIMINARY; PRT; 25 AA. SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=LIVER; RA Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases. DR U24278; AAA91124.1; FT NON_TER 25 ; SEQUENCE 25 AA; 2458 MW; 4D78687ACF623E59 CRC64; Qy 3 AALPRLIA 10 Db 4 AALPRASA 11	Score 25; DB 12; Length 25; Best Local Similarity 20.0%; Pred. No. 3.8e+0; Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;	RESULT 21 Q16158; ID Q16158; AC Q16158; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-JUN-2000 (TREMBLrel. 01, Last sequence update); DE C-MYC PROTEIN (FRAGMENT). OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. NCBI_TAXID=9606; [1]	PRELIMINARY; PRT; 15 AA. SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=LIVER; RA Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases. DR U24278; AAA91124.1; FT NON_TER 25 ; SEQUENCE 25 AA; 2458 MW; 4D78687ACF623E59 CRC64; Qy 3 AALPRLIA 10 Db 4 AALPRASA 11	Score 25; DB 12; Length 25; Best Local Similarity 20.0%; Pred. No. 3.8e+0; Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Q64000; ID Q64000; AC Q64000; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update); DE VASOPRESSIN (FRAGMENT). OS Rattus norvegicus (Rat).	PRELIMINARY; PRT; 25 AA. SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=LIVER; RA Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases. DR U24278; AAA91124.1; FT NON_TER 25 ; SEQUENCE 25 AA; 2458 MW; 4D78687ACF623E59 CRC64; Qy 3 AALPRLIA 10 Db 4 AALPRASA 11	Score 25; DB 12; Length 25; Best Local Similarity 20.0%; Pred. No. 3.8e+0; Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;	RESULT 21 Q16158; ID Q16158; AC Q16158; DT 01-NOV-1996 (TREMBLrel. 01, Created); DT 01-JUN-2000 (TREMBLrel. 01, Last sequence update); DE C-MYC PROTEIN (FRAGMENT). OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. NCBI_TAXID=9606; [1]	PRELIMINARY; PRT; 15 AA. SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=LIVER; RA Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases. DR U24278; AAA91124.1; FT NON_TER 25 ; SEQUENCE 25 AA; 2458 MW; 4D78687ACF623E59 CRC64; Qy 3 AALPRLIA 10 Db 4 AALPRASA 11	Score 25; DB 12; Length 25; Best Local Similarity 20.0%; Pred. No. 3.8e+0; Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RA Mertelsmann R.; Herrmann F.;
 RT "Burkitt-like mutations in the c-myc gene locus in prolymphocytic
 RL leukaemia";
 DR EMBL; S70386; AB30748.1; -;
 FT NON_TER 15 AA; 15 MW; 883FB769FC6D5A98 CRC64;

Query Match 19.2%; Score 24; DB 4; Length 17;
 Best Local Similarity 36.4%; Pred. No. 3.7e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 IPRLAFTSER 15
 ID :||| :||| :
 Db 1 MPLNVSFTSRN 11

RESULT 22
 Q9UC55 PRELIMINARY; PRT; 16 AA.
 ID Q9UC55
 AC Q9UC55;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE PROTEIN C OSAKA 10 (FRAGMENT).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96124381; PubMed=8560401;
 RA Miyata T., Zheng Y.Z., Sakata T., Kato H.;
 RT Protein C Osaka 10 with aberrant propeptide processing: loss of
 anticoagulant activity due to an amino acid substitution in the
 protein C precursor.;
 RT Thromb. Haemost. 74:1003-1008(1995).
 RL Raemost.
 SQ SEQUENCE 16 AA; 1875 MW; EBDP581FF3D325244 CRC64;

Query Match 19.2%; Score 24; DB 4; Length 16;
 Best Local Similarity 38.5%; Pred. No. 3.4e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 AETSESHFSIKR 22
 ID :||| :||| :|||:
 Db 4 SFLEELRHSSIER 16

RESULT 23
 Q9BYF2 PRELIMINARY; PRT; 17 AA.
 ID Q9BYF2
 AC Q9BYF2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE RIBOSMAL PROTEIN L39 (FRAGMENT).
 GN RPL39.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Uechi T., Tanaka T., Kenmochi N.;
 RT "A complete map of the human ribosomal protein genes: assignment of 80
 genes to the cytogenetic map and implications for human disorders.;"
 RL Genomics 72:23-220 (2001).
 DR EMBL; AB046411; BA021257.1;
 FT NON_TER 17 AA; 17 MW; 8398CFA38BD5FA9A CRC64;

Query Match 19.2%; Score 24; DB 13; Length 20;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 FTSEHSHFSI 20
 ID :||| :||| :|||:
 Db 2 FGNTHNFRKL 11

Query Match 19.2%; Score 24; DB 5; Length 18;
 Best Local Similarity 50.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 SEHSHF 18
 ID SEHSHF 18
 AC OPSS15
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE CREATINE KINASE (EC 2.7.3.2) (FRAGMENT).
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8019;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9308077; PubMed=1449598;
 RA White K.C., Bobbitt P.C., Buschler D.D., Kenyon G.L.;
 RT "The principal islet of the coho salmon (Oncorhynchus kisutch) contains
 the BB isoenzyme of creatine kinase.;"
 RL J. Protein Chem. 11:489-494 (1992).
 DR HSSP; P00563; ZORK; 2425 MW; BFBC71D6D2A86E11 CRC64;
 SQ SEQUENCE 20 AA; 2425 MW; BFBC71D6D2A86E11 CRC64;

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